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HIGH MOLECULAR WEIGHT PROTEIN FIG. 1A. DNA SEQUENCE OF (HMM1)

\leftarrow	ACAGCGTTCT	CTTAATACTA	GTACAAACCC	ACAATAAAAT	ATGACAAACA
51	ACAATTACAA	CACCTTTTT	GCAGTCTATA	TGCAAATATT	TTAAAAAATA
101	GTATAAATCC	GCCATATAAA	ATGGTATAAT	CTTTCATCTT	TCATCTTTCA
1,51	TCTTTCATCT	TTCATCTTTC	ATCTTTCATC	TTTCATCTTT	CATCTTTCAT
201	CTTTCATCTT	TCATCTTTCA	TCTTTCATCT	TTCATCTTTC	ACATGCCCTG
251	ATGAACCGAG	GGAAGGGAGG	GAGGGGCAAG	AATGAAGAGG	GAGCTGAACG
301	AACGCAAATG	ATAAAGTAAT	TTAATTGTTC	AACTAACCTT	AGGAGAAAAT
351	ATGAACAAGC	TATATCGTCT	CAAATTCAGC	AAACGCCTGA	ATGCTTTGGT
401	TGCTGTGTCT	GAATTGGCAC	GGGGTTGTGA	CCATTCCACA	GAAAAAGGCA
451	GCGAAAAACC	TGCTCGCATG	AAAGTGCGTC	ACTTAGCGTT	AAAGCCACTT
501	TCCGCTATGT	TACTATCTTT	AGGTGTAACA	TCTATTCCAC	AATCTGTTTT
551	AGCAAGCGGC	TTACAAGGAA	TGGATGTAGT	ACACGGCACA	GCCACTATGC
601	AAGTAGATGG	TAATAAAACC	ATTATCCGCA	ACAGTGTTGA	CGATATCATT
651	AATTGGAAAC	AATTTAACAT	CGACCAAAAT	GAAATGGTGC	AGTTTTTACA
701	AGAAAACAAC	AACTCCGCCG	TATTCAACCG	TGTTACATCT	AACCAAATCT

FIG. 1B

GTTAATTGAC	GCGATATTGC	ATTGTGTGGG	CGGACGCGCT	AAGAAAAAGG	501
GTATCAGGCA	AACCATCAAT	AAAAAGGCTC	ACCTCTTTAG	AGCAAAGAAA	.451
GCATTCAATT	GGTAAAAAGG	GCGCGGCGAA	GCGGTGACGA	ACTTACCTTG	.401
AGGGGGAGAA	CAGGTAAAGA	ATCGACCTTT	AGGTGCAGTT	CATTAAAAAC	1351
GATAAAGTCA	GATTACAGGC	GCAAGCTGAT	GCTAAAGGCG	AAATCAGCAA	1301
TTTCCGCTCA	GGCGGTGTAA	AGCGGAAATT	AAGAGGGTGA	CTTTCCGCCA	1251
CAATATTGTT	ATAAAAGCGG	GTAAGCAAAG	TGCTGATTCT	GTAAACTTTC	1201
CGAAACCAAG	TGCCACTATT	ATGTCCGTGC	GGTAACATTA	TGCCAAAGGC	1151
GCGATATTT	GTCAATCTGG	AAATGAAGCG	CCGCGCCTGA	TACAGCATTG	1101
AACCATTACT	TAATAAACCC	ATCAGCGATA	AAAAATCACC	TCGCAGGGCA	1051
ATTTCTTTAC	TGGTGGCAGC	TTAGCGTAAA	GAGGGTGTGA	AGTGAAAAAC	1001
TTGGTGGCAA	GTAAATCTTA	AGACGGCAGT	CTGTCGGTAA	GGTTTAATTA	951
TGTGAATCAC	TCGCTGAAAT	GATAAAGCGC	GCAAACCAAA	TCACCTTCGA	901
GCGCGTAATT		TTTCTAACGA	ACGCTAGACA	TACGGCTTCT	851
CTAATGGCTT		TAAAGACGCA	. TCACAATAGG	CCAAATGGTA	801
ТТТААТСААС	GACAAGTCTT	GATTCTAACG	, AGGGATTTTA	CCCAATTAAA	751

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CCGGTGGTTT GCAATTGTTG	CGGGATCCGG ACATTAACAA TAACATCACT	GAGATTAACA AACAATTTAC GGGCGCAAGG	AAAGGAAGCA TCAAAAAGGT GACTGCAATT	TTTGAAGGGA ACCTAAAAAT ATTTAACCTC
TAGTGGTGAT ATCGCTAAAA CCGGTGGTTT ATTTATTCAT CAAAGACAAT GCAATTGTTG GACCCGGATA ATGTATCTAT TAATCAAAA	. 0 .4	TGGCGGCGTT GTGCAAACTT ATCTCACTCG	CGCCTTTGAG AAAGGAAGCA CCTCAGGCAA TCAAAAAGGT ACTGGCAGCG GACTGCAATT	CACAAATAAA ' CAATGGȚTTT ; ACTTACTGGA ?
			•	AATACGCTAT CACAAATAAA TTTGAAGGGA GTGAACATCT CAATGGȚTTT ACCTAAAAAT CAAAGGACGC ACTTACTGGA ATTTAACCTC
A ACGCTCAAGG FTCGGGGCATG GTGGTTGTTA	ACAGCAGGAC GCAGCAATAC GAATAGTGCC AGCACCCCAA ACACAACTCT TGAGAGTATA GCTAATCAAC GCATCTATGT	TGGAGTGAGG CACCGGTGAT GGGTTGATGT	TACAGGTCAA ATAATGTCTC	AGAACCAATA TTCAGGGAAA (ATGATAAATT (ATGATAAAATT (ATGATAAAAATT (ATGATAAAAAAAAAA
GGCAATATTA TGTGGAGACG ACGCCAAAGA	ACAGCAGGAC GAATAGTGCC ACACAACTCT GCTAATCAAC	CTTAACTCTT ACGATATTAC TCAGGCGGCT TAACATAAAC	ACCAAGTCAT TTTAGATTTA	CTTTAAATAT GAAAGTGGAT
1551 1601 1651	1701 1751 1801 1851	1901 1951 2001 2051	2101 2151 2201	2251

FIG.1C.

TG. 1D

							4/8	32									
SACHOOPS						ACATTTO TO A				111GAAGGAG	CGAAGGCAAT	CGGATTTTGA	ATTAATAGCG	AAATCTTACC	СТТТТААТСТ	ATTGCCAAAC	AAGCATCACC
CCTCACTATT					CAAACCCCCG	GTCAAGTTTA	TAGAGAAAGA	CAAGTTGAAG	TAGCCAAAAA AAACATAACC		1 AACAGAAAT.	CTTATCGGTT	AGATGTCATC	ATATAGCCGG	ACAAATTTCA		
GCGAGTTTAA	CTTACCCAGC	CTTTAATGTT	TAGGGATAAA	ATTTCAGTTT	CTCTAACGTC	TTTCAACAGG	GGCTTCTCAA	AACACTTTTG	TAGCCAAAAA		りつつりでするこうこと	TAACGTCACT	CTATTAAAAA	AATATTGTCA	CAAAGCTATC	AAGGCAATTC	
TCCGAGAGTG	TGCAGGCACA	AAGACACTAC	AAGGCACCAA	TAATGGAAAC	TCGCCTCATC	TACTTTAATG	AACAAAAACT	GAGGCAACAT	AAAGGCATTG	CTTTGGGTTC		ATAACAACGC	AAACCTTTAA	CGCTGGAGGC	ACGCTAATTT	TTTGACAACA	CTTTAAAGAC ATTGATAATT
CTTAAATGTT	GAAGCGATAG	TCATTCAACA	CTTTGACATC	ACGCATCATT	TTCACACTTC	AAATTCTAAA	CTTCAGGCTC	AATGCCACCG	AATGATTGGT	GTAACATCAC		GI"PACTATCA	CAACCATCAA AAACCTTTAA	GCAACCTTAC	GTTGAAAGTA	AGGCGGCTTG	GAGGGCTCG
2351	2401	2451	2501	2551	2601	2651	2701	2751	2801	2851		7 A O T	2951	3001	3051	3101	3151

FIG. 1E.

								5/	82								
	i	AIMAGCGCA ATATAACCAA	ACTGAAATGC	GATTTCTTCT	GTGTTGATGG	ACCATTAAAA	TTTCAATAAA	GTAACACCAA	CAGGTTAAAG	CAGCAAAGTG	ACAATAATGC	AATATTACTT	TACCACTAAA	TAACCGCTCA	TCTGTAACAC	GGGCAACACC	AGGCTCTAC
				GTAATCTCAC			ATATTTCAGG	TTAACTATTG	AACCTTTAAC CAGGTTAAAG	TGACACTACA		AGTAAACAAC				GCAATATTTC G	ACCACTTTGG CAGGCTCTAC
	GCTCCACTTA CCGCACTATT			, CAAAAAGAAG		CGACAGACAA	AATONOGO A			GGICACAAGG	CAACACTGAA GATAGCAGTG		TCTGCGACAA	AACCACTGGT AACGTGGAGA	GAATTGAGTC CAGCTCTGGC	CIIGCIGIAA (UGGTGCATTA A
											ATOUR DUR	Alcgangcaa aaaangraac		ATOTEN DATE) 5414660010
	ACCAACI'C	TAAAAACGGT	AAATTGGCGG	GACAAAATCA	GGAGAATTCC	CCAAAGAATT	GCAGAGATTA	TAGTGCTGAT	ATTCAAAAAT	GAAACATCCG	CGGCTTAACT	CTCACABACC	ACAGGTACA	AACAGGTAGT			
3201	i 1 1	3251	3301	3351	3401	3451	3501	3551	3601	3651	3701	3751	3801	3851	3901	3951	

FIG. 1F

	TUUUUUUU	11))	1			
	T K K K K K K K K K K K K K K K K K K K	A U U U U U U U U U U U U U U U U U U U	AATAATACAA	TATTGAGCCA	CTGTACGTTT	801
	GGAGTAAGTG	AGCTAAACTT	GAGAAGCGTT	GATGAAGAAA	AGATTTATCT	751
	AGAAGGTAAA	CGCATCCTTG	TGAAGCGAAA	ATGAAGTAAT	GCAAGCGTAG	701
	ACCGGGTATA	AATACATTCA	ATTGATGTGA	AGGCGTTAAA	TACTGTTAAA	651
	ATAAACACCG	AAAAAACGGT	ATATCATTTC	AATGGATTAA	AATCACAATA	601
	CTGGGGATTT	GTGAACATCA	CTCAAGCAGA	TCGCGACAAC	GGCAGCGTAA	551
	AAATGGCTCC	CAACCAACGC	GTGGTAAATG	TAACCACACA	CAGCATTGGG	501
	CTAAATGGCG	AGACGCTGAG	TTAACGCAAA	ACCTTGGTTA	AACCAGCGGT	451
-	ACATTAATGC	AAGGGTTCAA	AACTACCGTG	CAGGCACTTT	CTAAATACTA	1401
٠,	CAATGTGACA	TTAATGCCGC	GCAGGAAGTA	TGGTAGCGTT	CAGCTCAGGA	1351
	GTAAATCTTT	CAAGGGTCAG	TTACTTCAGC	AGTTCACACA	TACCGAAGCT	1301
	GCAAATTAAC	ACATCATCGG	AACCTTAACT	AAGGAGCTGC	AATGCGACAG	1251
		TTGGGAATGG	GATTTAACAG	AAACGCTGGC	ATGTTACGGC	1201
		GATTTCCGGT	TTGGTGGTAC	ACAGGTACAA	AACAAGTGCA	4151
		ACAACAGGCG	AATTAAAGCA	CCAATTCAAA	ACCACTCAAT	4101
		TTAAAGCAAC	ACAGTAGAGG	TTCTGGTGGC	GCGGTACGAT	4051
	GGCGATATCG	AAGTCAATCA	TAACCACTTC	ACCGAGAGTG	AATTAAAGGA	4001

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FIG. 1G

				ACAGGTTATA	5101
AGTATTTTA	AATACAATAA	AATTACGGAG	ACCCA TCTTGTAAAA AATTACGGAG AATACAATAA AGTATTTTA	GCTTTACCCA	5051
TTCAGTACGG	TGGGTTAAAG	ATTTACTGTG	AGTCATTTTA TTTTCGTATT ATTTACTGTG TGGGTTAAAG TTCAGTACGG	AGTCATTTTA	5001
CCTGCAATGA	TAGATTTCAT	ATTGACAAGG	GGGTA GCGGTCAGTA ATTGACAAGG TAGATTTCAT CCTGCAATGA	ACGGGCGGTA	4951
ATCGCTGATA	GTGCGTTAAT	GCGCGACGGT	GTGTTTCTCA AACAGTGATG GCGCGACGGT GTGCGTTAAT ATCGCTGATA	GTGTTTCTCA	4901
AAGGCAGGGC	GTGATTTCTG	AAGTCGAATA	GAATTTGCAA CCAGACCATT AAGTCGAATA GTGATTTCTG AAGGCAGGGC	GAATTTGCAA	4851

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WEIGHT MOLECULAR HIGH 년 O SEQUENCE FIG. 2A. AMINO ACID PROTEIN

KVRHLALKPL DSNGQVFLIN DFDNVSINAE GTITSGNOKG IIRNSVDAII ISDIINPTIT IDLSGKEGGE IVWGDIALID LKKGTFVNIT DKALAEIVNH VSKDKSGNIV DTRGANLTIY VNISMVLPKN LTQPYNLNGI ISVSGGGSVD EKGSEKPARM FEGTLNISGK ARNFTFEQTK DKVTLKTGAV EINNDITTGD DSRGSDSAGT ISLLAGOKIT VSGKEKGGRA KGSNQVITGQ ATMOVDGNKT NQISQLKGIL RNQGKLSADS TLTNTTLESI AIVDAKEWLL SLNYASFNGN ELARGCDHST EGVISVNGGS LQGMDVVHGT NSAVFNRVTS TLDISNENIK AKGGKLMITG TSLEKGSTIN STPKRNKEKT WSEGRSGGGV ITAKQDIAFE RTNKYAITNK KAPIGINKYS GNINVRAATI SGHDLFIKDN SESGEFNLTI KRLNALVAVS SIPQSVLASG EMVQFLQENN VNLIGGKVKN GGVISAQNQQ IINTNGFTAS VNLGDIFAKG GKNGIQLAKK TGSGLOFTTK IAKTGGFVET INLSNGSLTL DEYTGSGNSA ISLGAQGNIN TYWNLTSLNV ERNARVNFDI MNKIYRLKFS FRFNNVSLNG PNGITIGKDA GLITVGKDGS YSIAAPENEA TYLGGDERGE GNINAQGSGD SAMLLSLGVT NWKQFNIDQN TAGRSNTSED ANORIYVNSS SGGWVDVHKN ESGYDKFKGR SFNKDTTFNV LSAKEGEAEI 51 101 151 201 301 57 351 451 401 501 551 601 701 651

IG.2B.

COLTL	N. F.	T. I.V.C.	TIST.	SSIL	GFNK		9/82 XLLI	SGNT	TESL	GAEI	ANVT	ANGS	OPGI	~ NOLC	
GFSIEKDLTL			IDNSKNLSTT	OKEGNLTISS	QDLNISGFNK	GHKVTLHSKV	SATSGEITTK	LAVSNISGNT	TVEVKATESL	DLTVGNGAE	AGSINAANVT	VVNATNANGS	IDVKYIOPGI	NNTITVDTON	
RFKTSGSTKT	FEGGNITFGS	INSGNLTAGG	IAKGGARFKD	TEMQIGGDVS	TIKTKELKLT	QVKDSKISAD	NITSHKAVSI	SVTLTATEGA	GDIGGTISGG	NTVNVTANAG	VNLSAQDGSV	LNGAALGNHT	INTVLLKGVK	GVSAVRFIEP	IADNGR
YFNVSTGSSL	KGIVAKKNIT	KPLTIKKDVI	FDNKGNSNIS	DLNITNEGSD	DSDATNNANL	GTNAKKVTFN	IDAKNVTVNN	ILGGIESSSG	TESVTTSSQS	TGTIGGTISG	SSHITSAKGQ	TLVINAKDAE	NGLNIISKNG	DEEREALAKL	NSDGATVCVN
QTPGVVINSK	QVEGTDGMIG	LIGSDFDNHQ	TNFTFNVGGL	ISGNITNKNG	IKAGVDGENS	LTIGNTNSAD	DSSDNNAGLT	NVEITAQTGS	TTLAGSTIKG	TTGEANVTSA	TSSGKLTTEA	KGSNINATSG	VNITGDLITI	RILEKVKDLS	VISEGRACFS
FTLLASSSNV	NATGGNITLL	VTINNNANVT	VESNANFKAI	TNSSSTYRTI	DKINITKQIT	AEITAKDGSD	ETSGSNNNTE	TGTTINATTG	VTVTANSGAL	TTQSNSKIKA	NATEGAATLT	LNTTGTLTTV	GSVIATTSSR	ASVDEVIEAK	EFATRPLSRI
T C /	801	851	901	951	001	051	101	151	201.	251	301	351	101	151	501

FIG.3A.

DNA SEQUENCE OF HIGH MOLECULAR WEIGHT

PROTEIN II (HMW2)

10/82 AATAAATCAA GATTTTTGTG ATGACAAACA TTAAAAAAT GGAGCTGAAC CACATGAAAT TAGGAGAAAA TTCATCTTTA TCATCTTTCA AATGCTTTGG ACCATTCCAC AGAAAAGGC TAAAGCCACT CAATCTGTTT AGCCACTATG ACGCTATCAT TAACCAAATC CAGTTTTTAC GAATGAAGAG CAAACGCCTG CACTTAGCGT TGCAAATATT TCTTTCATCT CTTTCATCTT TTTCATCTTT CAACTAACCT ATCTATTCCA TACACGGCAC AACAGTGTTG TGAAATGGTG GTGTTACATC CATCTTTCAT TGAATTGGCA CGGGGTTGTG CAACTCCGCC GTATTCAACC GCAGTCTATA AATGGTATAA ATCTTTCATC GATGAACCGA GGGAAGGGAG GGAGGGGCAA TCAAATTCAG TAGGTGTAAC TAGGTGTAAC CATTATCCGC TTTAATTGTT CTTACAAGGA ATGGATGTAG TCGACCAAAA AGATAATAAA CGCCATATAA TTTCATCTTT CACCTTTTTT TTCATCTTTC TTACTATCTT GATAAAGTAA ATATATCGTC TTACTATCTT GTAÄTAAAAC CAATTTAACA TAAATATACA ACAATTACAA AGTATAAATC TCTTTCATCT TTGCTGTGTC TAGCAAGCGG ATCTTTCATC SAACGCAAAT TATGAACAAG TTCCGCTATG TTCCGCTATG CAAGTAGATG TAATTGGAAA AAGAAAACAA \leftarrow 1 51 101 151 201 251 301 51 401 451 501 551 601 651 701

FIG.3B

						1	1/82								•
TTTTAATCAA	ACTAATGGCT	GGCGCGTAAT	TTGTGAATCA	ATTGGTGGCA	CATTTCTTTA	CAACCATTAC	GGCGATATTT	TCGAAACCAA	GCAATATTGT	ATTTCCGCTC	CGATAAAGTC	AAGGGGGAGA	GGCATTCAAT	TGTATCAGGC	CGTTAATTGA
GGACAAGTCT	AATTATTAAC	AAAACATCAA	CTCGCTGAAA	TGTAAATCTT	ATGGTGGCAG	ATAATAAACC	GGTCAATCTG	CTGCCACTAT	GATAAAAGCG	TGGCGGTGTA	TGATTACAGG	TCAGGTAAAG	AGGTAAAAAC	CAACCATCAA	GGCGATATTG
AGATTCTAAC	GTAAAGACGC	ATTTCTAACG	AGATAAAGCG	AAGACGGCAG	ATTAGCGTAA	CATCAGCGAT	AAAATGAAGC	AATGTCCGTG	TGTAAGCAAA	AAGCGGAAAT	GGCAAGCTGA	TATCGACCTT	AGCGCGGCGA	GAAAAAGGCT	TATTGTGTGG
AAGGGATTTT	ATCACAATAG	TACGCTAGAC	AGCAAACCAA	ACTGTCGGTA	CGAGGGTGTG	AAAAAATCAC	GCCGCGCCTG	CGGTAACATT	CTGCTGATTC	AAAGAGGGTG	AGCTAAAGGC	CAGGTGCAGT	GGCGGTGACG	AACCTCTTTA	GCGGACGCGC
TCCCAATTAA	CCCAAATGGT	TTACGGCTTC	TTCACCTTCG	CGGTTTAATT	AAGTGAAAAA	CTCGCAGGGC	TTACAGCATT	TTGCCAAAGG	GGTAAACTTT	TCTTTCCGCC	AAAATCAGCA	ACATTAAAAA	AACTTACCTT	TAGCAAAGAA	AAAGAAAAAG
751	801	851	901	951	1001	1051	1101	1151	1201	1251	1301	1351	1401	1451	1501

FIG. 3C

1551	CGGCAATATT		AACGCTCAAG GTAGTGGTGA	TATCGCTAAA	TATCGCTAAA ACCGGTGGTT	
1601	TTGTGGAGAC	ATCGGGGCAT	TATTTATCCA	TTGACAGCAA	TGCAATTGTT	
1651	AAAACAAAAG	AGTGGTTGCT	AGACCCTGAT	GATGTAACAA	TTGAAGCCGA	
1701	AGACCCCCTT	CGCAATAATA	CCGGTATAAA	TGATGAATTC	CCAACAGGCA	
1751	CCGGTGAAGC		AAGCGACCCT AAAAAAATA GCGAACTCAA AACAACGCTA	GCGAACTCAA	AACAACGCTA	
1801	ACCAATACAA		CTATTTCAAATTATCTGAAA AACGCCTGGA CAATGAATAT	AACGCCTGGA (CAATGAATAT	
1851	AACGGCATCA	AGAAAACTTA	CCGTTAATAG	CTCAATCAAC	ATCGGAAGCA _	1
1901	ACTCCCACTT	AATTCTCCAT	AGTAAAGGTC	AGCGTGGCGG	AGGCGTTCAG 8	2/82
1951	ATTGATGGAG	ATATTACTTC	TAAAGGCGGA	AATTTAACCA	TTTATTCTGG	
2001	CGGATGGGTT	GATGTTCATA	AAAATATTAC	GCTTGATCAG	GGTTTTTAA	
2051	ATATTACCGC	CGCTTCCGTA	GCTTTTGAAG	GTGGAAATAA	CAAAGCACGC	
2101	GACGCGGCAA	ATGCTAAAAT	TGTCGCCCAG	GGCACTGTAA	CCATTACAGG	
2151	AGAGGGAAAA	GATTTCAGGG	CTAACAACGT	ATCTTTAAAC GGAACGGGTA	GGAACGGGTA	
2201	AAGGTCTGAA	TATCATTTCA	TCAGTGAATA	ATTTAACCCA CAATCTTAGT	CAATCTTAGT	
2251	GGCACAATTA	ACATATCTGG	GAATATAACA	ATTAACCAAA	CTACGAGAAA	
2301	GAACACCTCG	TATTGGCAAA	CCAGCCATGA	TTCGCACTGG	AACGTCAGTG	
2351	CTCTTAATCT	AGAGACAGGC	GCAAATTTTA CCTTTATTAA ATACATTTCA	CCTTTATTAA	ATACATTTCA	

FIG.3D

						1	3/82								
CAGGGGTGAA	GAAGGAĞCGA	AAGCAAACCT	GGGCTCTGT	GAGTTAAAAA	AAATTCCCAT	CCATAAATGC	TTTATGACG	CATTCTGGGC	TTACGGGGAA	AATAACGCCC	CAGCTTGCTC	TTAAAGGCAA	AGAGATACCC	AATTAATATA	GTGATTTAAA
AGAAGCTCTG	CAATCTCAAA	ACATGAACAC	GCCACTGGTG	CAGAGGGGCT	ATTTTACCTT	AAAGACTTAA	GAAAGATGAT	ACAACATATC	AGCAGCAGCA	GCTAGAAGCC	TAAAACTTGG	AATGCAGATA	AGGAAAGACT	GCACTGCCGA	ACCAATGATG
AACACAGTAT	ACATGTCATT	CCAAACGAGA	CAATATCACA	ACCATTCTGG	AACGGCGCTA	TAAAATCAAC	TCAGACAGAC	AATTCAACCT	ACAAAACTCA	CAAATGTTAC	GATAGAGTTA	AACTGGCGAA	CCACTTTTAA	ACCAATAA†G	TGGCAATGTT
AAGGCTTAAC	GTAAATGGCA	CAAATTAAAA	GGTTTTTAGC	ATATATGCCA	TAATATCTCT	ATGACGCTTT	AATTTCAGCC	CAATGCCATC	CCCTTGGTGG	GAGAAAGCAG	AAACATAAGG	GTTTAAGTTT	TCAGAAAGCG	CGGCAATTTT	TGGTAAAACT
AGCAATAGCA	TTTTAACGGC	AAGTTAATTT	TTACCAATTC	TTTTTTGAT	TGAGTGAAAT	GTTCGCGGCG	AACCAATTCA	GGTACGCACG	GGTAATGTCA	TATTACTATC	CTAATCAGCA	GTTAATGGGA	TCTCACTATT	TAAATATCAC	ACACAAGGAG
2401	2451	2501	2551	2601	2651	2701	2751	2801	2851	2901	2951	3001	3051	3101	3151

TG. SE

							14/8:	2							
GGCGGAGATA	TAATGATGCT	ACCTCACGAT	AAAAAGGGTA	CAACCTAACT	TTTCAGGTTT	ACTATTGGCA	AACTTTTAAC	TGACACTAAA	AGCAATAGCG	AGTAAACAAA	AAAAGGTTAC	GCAAGTATTA	CACGGTAAGT	AAATTGAAGC	ATTGGCGGTA
AAGCATCATC	CAGACAGTAA	AAAGAAGGCA	GATAACAATC	CAAGTAATGC	GACCTAAGTA	TAGAGATTTA	CCAAAACAGT	GGTCACAATG	CGGACGTGAA	AAAATGTAGA	ACCGCGTCGG	AAATGGCAAA	TTTCCGGTAA	TCCGGCTCAA	AACAGGTACA
GCAACCAAAG	TTAAATATTA	TATCTCGCAA	TCACCAAACA	TCAGATGCGA	ATTGACAGAA	CCAAAGAŢGG	GGTGCCGAAG	CTCTGCTGAC	GCAGCAATGG	ATTACTGCAA	AGTAAATATC	TTAACGCAAC	AGCGGTACGA	AACCACTAAA	TAACAAGTGC
CATTACCACT CACGCTAAAC	AAAAGGAAGC	TTGGCGGCAA	AAAATTAATA	GGACTCTAGT	AAGAATTGAA	GAGATTACAG	CGGTAACAGC	ATTCAAAAAT	AAAACATCTA	CGGCTTAACT	CTCTCAAAAC	GGCTCGACCA	AGGTGATATC	CTGGTGATTT	GAGGCTAATG
CATTACCACT	TAATCAACAA	GAAATCCAAA	TTCTTCCGAT	TTGATGGAGA	ATTAAAACCA	CAATAAAGCA	ACAGTAATGA	AATGTTAAAG	TAGCAAAGTG	ACAACGATAC	GATATTACTT	CACCACAGCA	CAACCAAAAC	GTTAGCGCGA	GAAATCGGGT
3201	3251	3301	3351	3401	3451	3501	3551	3601	3651	3701	3751	3801	3851	3901	3951

FIG. 3F.

							15/	82								
CGATTTAACA	CAACCTTAAC				ATTAACGCAA	AGAAGTGAAT	CCTCAAGCAG	AATATCATTT	AATTGAGGTG	TTGAAGCGAA	AGAGAAACAT	AAATAATACA	CAAGTCAAGT	GGCGCACGAG	AATTGACAAG	TATTTACTGT
CAAACGCTGG	GAAGGAGCTG	CGGTTCTAGC	ATGGTAGCAT	ACAGGCACCT	CACCTTGGTT	GTGATAGTAC	ACTGCGGCAA	AAATGGGTTA	GAGGCAAGGA	GAAGAAGTAA	TGATGAAGAA	TTGTTGAGCC	ACCAGACCGT	AAGTGGTAAT	CGTAGTCAGT	ATTTTCGTAT TATTTACTGT
AATGTTACGG	TAATGCGACA	CTACTGAAGC	TTGGCTCAGA	ATTAAATACT	CAACCAGCGG	GATGCATCAG	TGGTAGTGTG	TAAACACAGT	GTGCGCTTAA GAGGCAAGGA	AGCAAGTGTA	AAGATTTATC	GCTGTACGTT	TGAATTTACA	CGTGTTTCTC	GATGGACAGC	AAGTCATTTT
TAATACGGTA	GCGCAGAAAT	AATACCTTGA	GGTAGACCTC	CTAATGTGAC	GATATTAAAG	AAGATGCTAA GCTAAATGGT	CAAGCGGCTC	ACTGGGGATT	TAGAAACACT	AGCCAGGTGT	GAAAAAGTAA	TGGTGTAAGT	ATACACAAAA	GAAGGTAAGG	TGTTGCTGAC	TCCTGCAATG
CAATTTCCGG	GTTGGGAATG	CGCAACAGGG	CTAAGGGTCA	ATTAATGCTG	GGCAGGCTCG	AAGATGCTAA	GCAGTCAACG	TGTGAATATC	CGAAAGATGG	AAATATATCC	ACGCGTCCTT	TAGCTAAACT	ATTACAGTCA	GATAATTTCT	TATGTACCAA	GTAGATTTCA
4001	4051	4101	4151	4201	4251	4301	4351	4401	4451	4501	4551	1601	1651	1701	1751	1801

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FIG.3G.

GTGGGTTAAA GTTCAGTACG GGCTTTACCC ATCTTGTAAA AAATTACGGA GAATACAATA AAGTATTTTT AACAGGTTAT TATTATG 4851 4901

HIGH FIG. 4A. AMINO ACID SEQUENCE PROTEIN

					17/8	32								•
KVRHLALKPL	IIRNSVDAII	DSNGQVFLIN	DKALAEIVNH	ISDIINPTIT	VSKDKSGNIV	IDLSGKEGGE	IVWGDIALID	DFDNVSINAE	YLKNAWTMNI	KGGNLTIYSG	VAQGTVTITG	NITINQTTRK	TQYRSSAGVN	NITATGGGSV
EKGSEKPARM	ATMQVDGNKT	NQISQLKGIL	ARNFTFEQTK	ISLLAGQKIT	RNQGKLSADS	DKVTLKTGAV	VSGKEKGGRA	AIVDAKEWLL	TTLTNTTISN	GVQIDGDITS	KARDAANAKI	NLSGTINISG	YISSNSKGLT	SKPLPIRFLA
ELARGCDHST	LQGMDVVHGT	NSAVFNRVTS	TLDISNENIK	EGVISVNGGS	GNINVRAATI	AKGGKLMITG	TSLEKGSTIN	SGHDLFIKDN	SDPKKNSELK	ILHSKGQRGG	ASVAFEGGNN	IISSVNNLTH	ETGANFTFIK	KLKPNENMNT
KRLNALVAVS	SIPQSVLASG	EMVQFLQENN	IINTNGFTAS	VNLIGGKVKN	VNLGDIFAKG	GGVISAQNQQ	GKNGIQLAKK	IAKTGGFVET	DEFPTGTGEA	SINIGSNSHL	LDQGFLNITA	SLNGTGKGLN	SHWNVSALNL	NLKEGAKVNF
MNKIYRLKFS	SAMLLSLGVT	NWKQFNIDQN	PNGITIGKDA	GLITVGKDGS	YSIAAPENEA	LSAKEGEAEI	TYLGGDERGE	GNINAQGSGD	DPLRNNTGIN	TASRKLTVNS	GWVDVHKNIT	EGKDFRANNV	NTSYWQTSHD	FNGVNGNMSF
⊣	51	101	151	201	251	301	351	401	451	501	551	601	651	701

FIG. 4B.

			VADDGQP	SGNGARVCTN	IISEGKACFS	451
	EFTTRPSSQV	NNTITVNTON	GVSAVRFVEP	DEERETLAKL	RVLEKVKDLS	401
	ASVEEVIEAK	IEVKYIQPGV	RNTVRLRGKE	NGLNIISKDG	VNITGDLNTV	.351
	GSVTAATSSS	EVNAVNASGS	LNGDASGDST	TLVINAKDAK	AGSDIKATSG	301
	LNTTGTLTTV	AGSINAANVT	VDLLAQNGSI	GSSITSTKGQ	ATGNTLTTEA	.251
	NATEGAATLT	DLTVGNGAEI	NTVNVTANAG	TGTIGGTISG	KSGEANVTSA	201
	TTKSGSKIEA	TVSVSATVDL	GDISGTISGN	NGKASITTKT	TTAGSTINAT	1151
<i>-</i>	VNITASEKVT	VNKDITSLKT	GLTITAKNVE	GRESNSDNDT	SKVKTSSSNG	1101
	SADGHNVTLN	TFNNVKDSKI	GNSGAEAKTV	RDLTIGNSND	NKAEITAKDG	1051
	LTEDLSISGF	NLTIKTKELK	DSSSDATSNA	ITIKKGIDGE	SSDKINITKQ	1001
	ISQKEGNLTI	NDAEIQIGGN	KGSLNITDSN	SIIGGDIINK	ITTHAKRNQR	951
	GNVTNDGDLN	INITQGVVKL	GNFTNNGTAE	GKTRDTLNIT	. LTISESATFK	901
	TGENADIKGN	SLLVNGSLSL	NIRDRVIKLG	LEANNAPNQQ	ITIEKAANVT	851
	QNSSSSSTTGN	ILGGNVTLGG	NAINSTYNIS	KDDFYDGYAR	TNSNFSLRQT	801
	KINKDLTINA	NSHVRGDDAF	NISNGANFTL	RGAELKMSEI	FFDIYANHSG	751

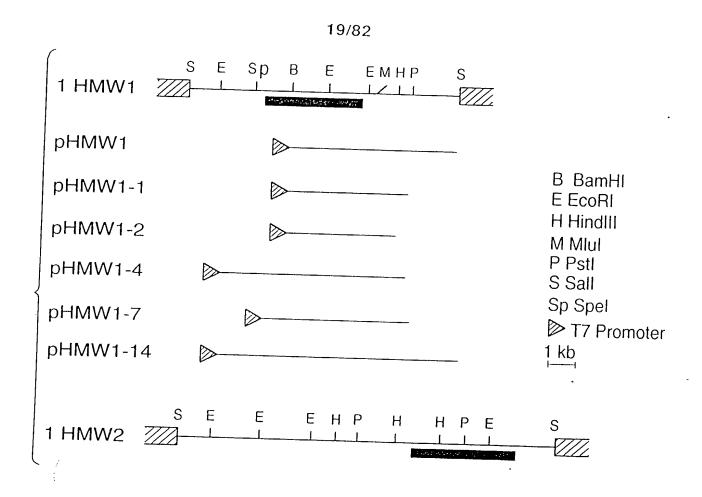
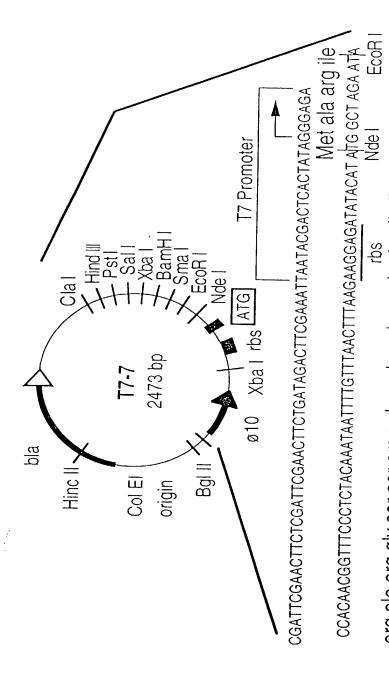


FIG.5A.





arg ala arg gly ser ser arg val asp leu gln pro lys leu ile ile asp ...

F16.5B.

shaded boxes indicate the locations of the structural genes. In the recombinant phage, transcription proceeds from left to right for the HMW1 gene and from right to left for the HMW2 gene. The methods used for construction of the plasmids shown are (A) Partial restriction maps of representative HMW1 and HMW2 recombinant phage and of HMW1 plasmid subclones. The described in the text. (B) Restriction map of the T7 expression vector pT7-7. This vector contains the T7 RNA polymerase promoter 女10, a ribosome - binding site (rbs), and the translational start site for the T7 gene 10 protein upstream from a multiple cloning site (37).

FIG.6A.

ATGACAAACA TTAAAAAATA TCATCTTTCA CATCTTTCAT ACATGAAATG GAGCTGAACG AGGAGAAAAT ATGCTTTGGT GAAAAAGGCA AAAGCCACTT GCCACTATGC CGCTATCATT AATCTGTTTT AGTTTTACA AACCAAATCT TTTAATCAAC CTTAATACTA GTACAAACCC ACAATAAAAT CTTTCATCTT AATGAAGAGG TGCAAATATT TTTCATCTTT TTCATCTTTC AACTAACCTT AAACGCCTGA CCATTCCACA ACTTAGCGTT ACACGGCACA TCTATTCCAC ACAGTGTTGA GAAATGGTGC TGTTACATCT GACAAGTCTT GCAGTCTATA ATGGTATAAT GAGGGCCAAG ATCTTTCATC TCTTTCATCT CAAATTCAGC TTAATTGTTC GGGGTTGTGA AAAGTGCGTC TGGATGTAGT ATTATCCGCA AGGTGTAACA CGACCAAAAT TATTCAACCG GATTCTAACG CACCTTTTTT TCATCTTTCA GCCATATAAA TTCATCTTTC GGAAGGGAGG ATAAAGTAAT TATATCGTCT GAATTGGCAC AATTTAACAT TACTATCTTT TGCTCGCATG TAATAAAACC TTACAAGGAA AACTCCGCCG AGGGATTTTA ACAATTACAA ACAGCGTTCT STATAAATCC TCTTTCATCT CTTTCATCTT ATGAACCGAG ATGAACAAGA AACGCAAATG TGCTGTGTCT AATTGGAAAC GCGAAAAACC TCCGCTATGT AGCAAGCGGC AAGTAGATGG AGAAAACAAC CCCAATTAAA \vdash 51 101 201 151 251 301 351 401 451 501 551 601 651 701 751

FIG. 6B.

	GCAATTGTTG	CAAAGACAAT GCAATTGTTG	ATTTATTCAT	TCGGGGCATG	TGTGGAGACG	601
	CCGGTGGTTT	ATCGCTAAAA	TAGTGGTGAT	ACGCTCAAGG	GGCAATATTA	551
	GTTAATTGAC	GCGATATTGC	ATTGTGTGGG	CGGACGCGCT	AAGAAAAAGG	501
	GTATCAGGCA	AACCATCAAT	AAAAAGGCTC	ACCTCTTTAG	AGCAAAGAAA	451
	GCATTCAATT	GGTAAAAACG	GCGCGGCGAA	GCGGTGACGA	ACTTACCTTG	401
	AGGGGGAGAA	CAGGTAAAGA	ATCGACCTTT	AGGTGCAGTT	CATTAAAAAC	351
	GATAAAGTCA	GATTACAGGC	GCAAGCTGAT	GCTAAAGGCG	AAATCAGCAA	301
_	TTTCCGCTCA	GGCGGTGTAA	AGCGGAAATT	AAGAGGGTGA	CTTTCCGCCA	251
	CGAAACCAAG	TGCCACTATT	ATGTCCGTGC	GGTAACATTA	TGCCAAAGGC	151
	GCGATATTT	GTCAATCTGG	AAATGAAGCG	CCGCGCCTGA	TACAGCATTG	101
	AACCATTACT	TAATAAACCC	ATCAGCGATA	AAAAATCACC	TCGCAGGGCA	.051
	ATTTCTTTAC		TTAGCGTAAA	GAGGGTGTGA	AGTGAAAAAC	1001
			AGACGGCAGT	CTGTCGGTAA	GGTTTAATTA	951
			GATAAAGCGC	GCAAACCAAA	TCACCTTCGA	901
				ACGCTAGACA	TACGGCTTCT	851
	CTAATGGCTT	ATTATTAACA	TAAAGACGCA	TCACAATAGG	CCAAATGGTA	801

. 6C.

CAAGAGTCAA	GAACGAAATG (CTTTAATGTT		17)1111)	
AAACGGTATA ·				TCATTCAACA AAGAAAAAAAA	451
GACICAGAG			TGCAGGCACA (GAAGCGATAG	401
		CAAAGGACGC	ATGATAAATT	GAAAGTGGAT	351
	ACTTACTGGA	CAAAGGACGC	ATGATAAATT	GAAAGI'GGAT	H O (
ACCTAAAAAT		1) 11701 - 1	1		301
T I GARGGGA		GTGAACATCT	TTCAGGGAAA	CTTTAAATAT	251
	CACAAATAAA	AATACGCTAT	AGAACCAATA	CACCACTAAA	H ,
GACTGCAATT	ACTGGCAGCG	1 C TAAACGGC			2001
LOBBARAGG,I,	CH ())) ; ; ;	(((((((((((((((((((ATAATCTOTO	TTTAGATTTA	2151
		GGGACTATTA	TACAGGTCAA	ACCAAGTCAT	H O H V
	CGCCTTTGAG	AACAAGATAT	ATTACAGCTA	IAACATAAAC	, H () () () ()
GGGCGCAAGG	ATCTCACTCG	LOUIWARANI		E 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	2051
AACAA1"1"I'AC		E K K K K K K K K K K K K K K K K K K K	GGGTTGATGT	TCAGGCGGCT	2001
		GATACCAGAG	CACCGGTGAT	ACGATATTAC	1001
GAGATTAACA	TGGCGGCGTT	GTCGGAGCGG		1 1 1 1 1 1	C TT
CCAATGGCAG			77 47H7475H L	CTTAACTCTT	1901
		CAATAGCTCC	GCATCTATGT	GCTAATCAAC	T C O T
TAACACA	GTACCTTTGT	CI'AAAAAAG	WIWI DUDIN:		C C
ACATTAACAA	AGARARGACA		_	ACACACACTOR	1801
		AACGAAACAA	2 AGCACCCCAA	GAATAGTGCC	79/7
	GATGAATACA	: TTCAGAAGAC	GCAGCAATAC	PCAGCAGGAC.) ; ; ; ;
TAATGCAGAA	A ATGTATCTAT	A GAUCUGGATA		()	1701
			A GTGGTTGTT	ACGCCAAAGA	1651

FIG.6D.

AGTTTGAATT	GTGTAGTTAT	AGATTTAAAA TTTAACTTTA	GCACCGATGG	TTTGAAGGAG	CGAAGGCAAT	CGGA'I'TTTGA	A'I''I'AATAGCG	AAA'I'C'I'TACC		AAGCATCACC	ATATAACCAA	ACTGAAATGC
TAAGTATTCT CGGGAGGGG		G'I'CAAGTTTA A TAGAGAAAGA T			TAACAGAAAT. C.			ACAAATTTA			•	•
TAGGGATAAA	CTCTAACGTC	GGCTTCTCAA	AACACTTTTG	AGGAAAGCCA				,		ATTGATAATT C	CCGCACTATT A	TTACGAACGA AGGTAGTGAT
S AAGGCACCAA P TAATGGAAAC	TCGCCTCATC		GAGGCAACAT AAAGGCATTG			AAACCTTTAA	CGCTGGAGGC	ACGCTAATTT	TTTGACAACA	CTTTAAAGAC	GCTCCACTTA	GATTTAAATA
CTTTGACATC ACGCATCATT	TTCACACTTC AAATTCTAAA	CTTCAGGCTC	AATGATTGGT	GTAAGATGAG	GTTACTATCA	CAACCATCAA	GCAACCTTAC	GTTGAAAGTA	AGGCGGCTTG	GAGGGCTCG	ACCAACTCCA	TAAAAACGGT
2501	2601 2651	2701	2801	2851	2901	2951	3001	3051	101	157	201	797

FIG.6E

3301	AAATTGGCGG	GATGTCTCG	CAAAAAGAAG	GTAATCTCAC	GA TTTCTTCT
3351	GACAAAATCA	ATATTACCAA	ACAGATAACA		
3401	GGAGAATTCC	: GATTCAGACG			
3451	CCAAAGAATT	GAAATTAACG	CAAGACCTAA	ATATTTCAGG	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
3501	GCAGAGATTA	. CAGCTAAAGA	TGGTAGTGAT	TTAACTATTG	GTAACACCAA
3551	TAGTGCTGAT	GGTACTAATG	CCAAAAAAGT	AACCTTTAAC	CAGGTTAAAG
3601	ATTCAAAAAT	CTCTGCTGAC	GGTCACAAGG	TGACACTACA	CAGCAAAGTG
3651	GAAACATCCG	GTAGTAATAA	CAACACTGAA	GATAGCAGTG	ACAATAATGC
3701	CGGCTTAACT	ATCGATGCAA	AAAATGTAAC	AGTAAACAAC	AATATTACTT
3751	CTCACAAAGC	AGTGAGCATC	TCTGCGACAA	GTGGAGAAAT	TACCACTAAA
3801	ACAGGTACAA	CCATTAACGC	AACCACTGGT	AACGTGGAGA	TAACCGCTCA
3851	AACAGGTAGT	ATCCTAGGTG	GAATTGAGTC	CAGCTCTGGC	TCTGTAACAC
3901	TTACTGCAAC	CGAGGGCGCT	CTTGCTGTAA	GCAATATTTC	GGGCAACACC
3951	GTTACTGTTA	CTGCAAATAG	CGGTGCATTA	ACCACTTTGG	CAGGCTCTAC
1001	AATTAAAGGA	ACCGAGAGTG	TAACCACTTC	AAGTCAATCA	GGCGATATCG.
1051	GCGGTACGAT	TTCTGGTGGC	ACAGTAGAGG	TTAAAGCAAC	CGAAAGTTTA

FIG. 6F.

ACCACTCAAT	CCAATTCAAA	CCAATTCAAA AATTAAAGCA ACAACAGGCG AGGCTAACGT	ACAACAGGCG	AGGCTAACGT
	GCA ACAGGTACAA	TTGGTGGTAC	GATTTCCGGT	AATACGGTAA
	AAACGCTGGC	GATTTAACAG	TTGGGAATGG	CGCAGAAATT
	AAGGAGCTGC	AACCTTAACT	ACATCATCGG	GCAAATTAAC
	AGTTCACACA	TTACTTCAGC	CAAGGGTCAG	GTAAATCTTT
	TGGTAGCGTT	GCAGGAAGTA	TTAATGCCGC	CAATGTGACA
	CAGGCACTTT	AACTACCGTG	AAGGGTTCAA	ACATTAATGC ,
	ACCTTGGTTA	TTAACGCAAA	AGACGCTGAG	CTAAATGGCG 89
	TAACCACACA	GTGGTAAATG	CAACCAACGC	AAATGGCTCC
	TCGCGACAAC	CTCAAGCAGA	GTGAACATCA	CTGGGGATTT
AATCACAATA	AATGGATTAA	ATATCATTTC	AAAAACGGT	ATAAACACCG
TACTGTTAAA	AGGCGTTAAA	ATTGATGTGA	AATACATTCA	ACCGGGTATA
	ATGAAGTAAT	TGAAGCGAAA	CGCATCCTTG	AGAAGGTAAA
_	GATGAAGAAA	GAGAAGCGTT	AGCTAAACTT	GGCGTAAGTG
	TATTGAGCCA	AATAATACAA	TTACAGTCGA	TACACAAAAT
	CCAGACCATT	AAGTCGAATA	GTGATTTCTG	AAGGCAGGGC.
GTGTTTCTCA	AACAGTGATG	GCGCGACGGT	GTGCGTTAAT	ATCGCTGATA

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いりてはない	TTCAGTACGG	AGTATTTTA	CTCAGTGCAA	AGAAGAAGCG	CTTTAAGTGA	CAAGGCTCGC 22	GGCTGTGCTA 8	AACAAACCAT	GCCGCAGAAA	AAATATCGCT	ATGGTCGTCA	CCACTTAAAG	CTCTGATTTG	TTGTTTCCTA	AGTCTAGGTT
CCTGCAATGA	TTCAC	AGTAI	CTCAG	AGAAG		CAAGG	GGCTG		SCCGC		ATGGT	CCACT	CTCTG	TTGTT	AGTCT
	TGGGTTAAAG	AATACAATAA	CAGATTAAAA	CATTGTATGC	GCACTTGAAA	ATCTAAATAC	TTGAATTACA	ATATTGCCAC	CTCGAAATCA	ATAGTGAAGA	GTGTATGAAG	AAAAGAAAAT	TTAAACCCTA AAAACAAAAC	ACGCGTAGCT	TCAACGTGTA
מסטיייייייייייייייייייייייייייייייייייי	ATTTACTGTG	AATTACGGAG	ATATAAAAG	GCTTCTTCAT	GTTATCTGGT	CAAAATCTTT	ACAGCACAGC	GTTTGATGTG	TTGAGCTAGT	AGCCAGGGTT	ACAAGGAAAA	TCAATATGGC	TTAAACCCTA	TTTTGGCAAA	AGTTTAACTA
	TTTTCGTATT	TCTTGTAAAA	ATTATGAAAA	GCTTGGCCTG	AAGGCTTTCA	CTGTCTGTAG	AAACCTAAAA	AGCCAAATAA	AATATTATGT	TTATAAGGCG	CATCTTTGAA	TTGCGTGAAT	GCATTACGAG	GTTTTTCGCC	GGCGCAAGGG
	AGTCATTTTA	GCTTTACCCA	ACAGGTTATT	TATCAGTATT	TTTTTAGTAA	AGACGCCCAA	AAACTTTAAC	GATAAGATTG	TACGGATGGC	GCCAAGTTTT	CGTAGCCTGC	GTGGTTCGAT	TCACTCGCGT	GTAGTTGCAG	TGATAATTTC
H))	5001	5051	5101	5151	5201	5251	5301	5351	5401	5451	5501	5551	5601	5651	5701

FIG. 6H.

CTGCGGGTTT	ACGGTATCCT	AGATATGCAC	CTTACGGCGA	AATGCTAAAA	6551
TAATAGCGAA	AGTTCCGTTA	GATGCAGGTC	TGCGTTTTAT	TCAGCCCTTA	6501
CGCTTTCAAA	AAAATACACC	TAAGTATGCC	CGTAATGAAT	TCTTGTATGG	6451
GTGAGCGCGG	GGTGCAAGTG	TAAATACGGC	TCAGAGGCTT	ACTTATGGCG	6401
TGTAACAGGT	ATTTATTCTC	AGTAGCATAG	ACAAGATATA	AGTTTACTCT	6351
TTATCGGGTC	TAGCAGTCAA	GTTGGCATTT	TTTGCTCAAG	GAGTCAAGAG	6301
GTTTAGGGTT	AGCACAGCCA	CTATCACATT	TTAATCGCAG	GGCGAAACAT	6251
GGAGCGCATT	CTTTTGGAAT	TTACCAGGCT	CGCGAGTAAA	ATCATTATTA	6201
GATTTAACTC	CTTTAATATT	CTAAAACAAT	CAATTTACCC	TGGACATATC	6151
CAGGCATTGA	GGCGTAAGTG	TGCAGTATCA	AGAAAAATT	GGTGCAACGA	6101
AAACACCCTG	CATCCGAGTT	ATTAATCAAA	CTACCGCCAT	TAGGCTACAA	6051
AAAATTAATT	AGACCAGTTT	TTGGAATGGA	ACATTTAACC	TTATCTCCCG	6001
AATGGAGTTA	GCGAATCTGA	ATCTATCTCT	CAAAAGGTCA	CGTAAATTAT	5951
TGCGATTAAT	GCTTACCAAG	GATATCGACG	TGATTCTAAT	TGAGTTATGC	5901
TATACCAGCA	CTTAAGTCTT	AACACCAATC	TTTTATGATA	TACTTATCCG	5851
GCATAGGATA	TATGCGGTAG	ATCAAAATCT	TAAAAGCACC	TTGACCAATG	5801
TCTAAACGCA	ATGTATTAAA	CAATTTGACC GGACATGATG	CAATTTGACC	TTGTAAATGC	5751

FIG.61.

						2	29/82	2							
GCTTTTGTTG	CAACAAAAA		GTTTATAACT	GTTTCATCC	AAACCAAGCA		ATGCTAAAAA			TGCAAATACT	CATGTCGCCA	TTTGGAAAAA	ACGCACCTGC	GCCACTCGTC	
AAGCTTAGAT	ATTTGAATGG	AGATTAACAT	CCGCCTACCA	ACGCAACCCT		CCAAGCAAAC CAAGCAAACC AAGCAAACCA	CAAACCAAGC AAACCAAGCA	CATACCATGG	AAAGTGTTCC	CAAACTTCCC	CCTGGAACAA	TAATGGCGAT	ATTGAATTTG	AATTCATTTT	ACCCCGAATT
CACAAAACTT	AATAGTGACA	CTTCTGGGGT	GGTAAGCGTT	TACAGTCTAT	GCAAACCAAG	CCAAGCAAAC	CAAACCAAGC	AAACATACTC	GAAAATTTAC	TTGTAGAATC AAACAACGAC CAAACTTCCC	ACCTATTACG	TGCCGCGAAT	CGTTCACGAT	AAAAACTACT	CTCTTTTCCG
ACCTCTCCTA	TGCAAATGCC	CACCTACAAC	TTAATCAACT	CCCGCCAATT	AACAAACTAA	ACCAAGCAAA	GCAAACCAAG	TGATAAACTA	TATGACAAAA	TTGTAGAATC	CCCAAACCCA	TGAGCTTGCT	ATTTTGGAGG	TATCTACCCG	AATTACAACA CTCTTTTCCG ACCCCGAATT GGCAATTTCC
AGGCATTAAA	CTCGTCGCTT	CGCACAAGCT	ACCCTGAAAT	ATATGCTTTA	TTATATATCA	AACCAAGCAA	AGCAAACCAA	ACAATTTATA	GATTTAATAA	ACCGCTTCAC	TAAACAACCA	AAAAAGATTA	ATGGACGCTA	TCAGCTGGCA	TCGCTAATGC
6601	6651	6701	6751	6801	6851	6901	6951	7001	7051	7101	7151	7201	7251	7301	7351

FIG. 6J

7401	GAAGAAGGGG	CATTAAAGAT	GATTAGCCTG CAACGCTGGT	CAACGCTGGT	TGACGCTGAT
7451	TTTTGCCTCT	TCCCCCTACG	TTAACGCAGA	CCATATTCTC	AATAAATATA
7501	ATATCAACCC	AGATTCCGAA	GGTGGCTTTC	ATTTAGCAAC	AGACAACTCT
7551	TCTATTGCTA	AATTCTGTAT	TTTTTACTTA	CCCGAATCCA	ATGTCAATAT
7601	GAGTTTAGAT	GCGTTATGGG	CAGGGAATCA	ACAACTTTGT	GCTTCATTGT
7651	GTTTTGCGTT	GCAGTCTTCA	CGTTTTATTG	GTACTGCATC	TGCGTTTCAT
7701	AAAAGAGCGG	TGGTTTTACA	GTGGTTTCCT	AAAAACTCG	CCGAAATTGC
7751	TAATTTAGAT	GAATTGCCTG	CAAATATCCT	TCATGATGTA	TATATGCACT 8
7801	GCAGTTATGA	TTTAGCAAAA	AACAAGCACG	ATGTTAAGCG	TCCATTAAAC
7851	GAACTTGTCC	GCAAGCATAT	CCTCACGCAA	GGATGGCAAG	ACCGCTACCT
7901	TTACACCTTA	GGTAAAAAGG	ACGGCAAACC	TGTGATGATG	GTACTGCTTG
7951	AACATTTTAA	TTCGGGACAT	TCGATTTATC	GCACGCATTC	AACTTCAATG
8001	ATTGCTGCTC	GAGAAAAATT	CTATTTAGTC	GGCTTAGGCC	ATGAGGGCGT
8051	TGATAACATA	GGTCGAGAAG	TGTTTGACGA	GTTCTTTGAA	ATCAGTAGCA
8101	ATAATATAAT	GGAGAGACTG	TTTTTTATCC	GTAAACAGTG	CGAAACTTTC .
8151	CAACCCGCAG	TGTTCTATAT	GCCAAGCATT	GGCATGGATA	TTACCACGAT

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8201	TTTTGTGAGC	AACACTCGGC	TTGCCCCTAT	TCAAGCTGTA	GCCTTGGGTC
8251	ATCCTGCCAC	TACGCATTCT	GAATTTATTG	ATTATGTCAT	CGTAGAAGAT
8301	GATTATGTGG	GCAGTGAAGA	TTGTTTAGC	GAAACCCTTT	TACGCTTACC
8351	CAAAGATGCC	CTACCTTATG	TACCATCTGC	ACTCGCCCCA	CAAAAAGTG
8401	ATTATGTACT	CAGGGAAAAC	CCTGAAGTAG	TCAATATCGG	TATTGCCGCT
8451	ACCACAATGA	AATTAAACCC	TGAATTTTTG	CTAACATTGC	AAGAAATCAC
850.1	AGATAAAGCT	AAAGTCAAAA	TACATTTTCA	TTTCGCACTT	GGACAATCAA
8551	CAGGCTTGAC	ACACCCTTAT	GTCAAATGGT	TTATCGAAAG	CTATTTAGGT
3601	GACGATGCCA	CTGCACATCC	CCACGCACCT	TATCACGATT	ATCTGGCAAT
3651	ATTGCGTGAT	TGCGATATGC	TACTAAATCC	GTTTCCTTTC	GGTAATACTA
3701	ACGGCATAAT	TGATATGGTT	ACATTAGGTT	TAGTTGGTGT	ATGCAAAACG
3751	GGGGATGAAG	TACATGAACA	TATTGATGAA	GGTCTGTTTA	AACGCTTAGG
3801	ACTACCAGAA	TGGCTGATAG	CCGACACACG	AGAAACATAT	ATTGAATGTG
3851	CTTTGCGTCT	AGCAGAAAAC	CATCAAGAAC	GCCTTGAACT	CCGTCGTTAC
3901	ATCATAGAAA	ACAACGGCTT	ACAAAAGCTT	TTTACAGGCG	ACCCTCGTCC
951	ATTGGGCAAA	ATACTGCTTA	AGAAAACAAA	TGAATGGAAG	CGGAAGCACT
001	TGAGTAAAAA	ATAACGGTTT	TTTAAAGTAA AAGTGCGGTT	AAGTGCGGTT	AATTTCAAA

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FIG.6L.

GCGTTTTAAA AACCTCTCAA AAATCAACCG CACTTTTATC TTTATAACGC TAAAATTGTG GGTAATCAAA TTCAATTGTT GATACGGCAA ACTAAAGACG TCCCGCGCGC TGACAGTTTA TCTCTTTCTT AAAATACCCA GCGCGTTCTT CGGCAGTCAT C GCAATAGTTG 9051 9101 9151 9201

FIG. 7A.

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AAAGTGCGG	TAATTGTTCA	CTTTTTCGGT	ACAACTTTAC	GCGAATACGT	CATAATAGGT	TTTGCAAGAT	TTTTAATTCA	TAAATATACA	ACAATTACAA	AGTATAAATC	ATCTTTCATC	TCTTTCATCT	GATGAACCGA	GAACGCAAAT	
AACTAACCAA AAAGTGCGGT	AAGAACGAGG	GTTGGCGTTT	CAATCCACCA	GCTCTTCTTG	TCGGGATAAT	AATCATAAAT	AAATCGCCAA	ATCAACTGGT	ATGACAAACA	TTAAAAAAAT	TTCATCTTTC	TCATCTTTCA	CACATGAAAT	GGAGCTGAAC	TAGGAGAAA
GTTGAAATTC	GGTTGTAGTG	TTGGGCATTG	GACGACTATG	GTAAGTTCTT	AAGAAAATGA	GATGTTCTAA	ATTTGTGGCG	TCCCACTCAA	GATTTTTGTG	TGCAAATATT	TCTTTCATCT	CTTTCATCTT	TTTCATCTTT	GAATGAAGAG	CAACTAACCT
ATTTGGATT	GGAGAAAATA	GCTCTCTTAA	TTATATTCTG	AAGCGTTAAT	TTTGTTTAGC	AATAAATTTT	TTCAATACCT	GCATAATATT	AATAAATCAA	GCAGTCTATA	AATGGTATAA	CATCTTTCAT	ATCTTTCATC	GGAGGGGCAA	TTTAATTGTT
CGCCACTTCA	TAAAATCTGT	AAAGGATAAA	TAATAGTAAA	CGTTGGTTTT	AATCCCATTT	GTTGCCCAAA	ATTGTGGCAA	ATTTCTTGTA	AGATAATAAA	CACCTTTTTT	CGCCATATAA	TTTCATCTTT	TTCATCTTTC	GGGAAGGGAG	GATAAAGTAA
Н	51	101	151	201	251	301	351	401	451	501	551	501	551	701	751

FIG. 7B

TTGCCAAAGG	GGCGATATTT	GGTCAATCTG	AAAATGAAGC	GCCGCGCCTG	551
TTACAGCATT	CAACCATTAC	ATAATAAACC	CATCAGCGAT	AAAAAATCAC	501
CTCGCAGGGC	CATTTCTTTA	ATGGTGGCAG	ATTAGCGTAA	CGAGGGTGTG	451
AAGTGAAAAA	ATTGGTGGCA	TGTAAATCTT	AAGACGGCAG	ACTGTCGGTA	401
CGGTTTAATT	TTGTGAATCA	CTCGCTGAAA	AGATAAAGCG	AGCAAACCAA	.351
TTCACCTTCG	GGCGCGTAAT	AAAACATCAA	ATTTCTAACG	TACGCTAGAC	.301
TTACGGCTTC	ACTAATGGCT	AATTATTAAC	GTAAAGACGC	ATCACAATAG	.251
CCCAAATGGT	TTTTÅATCAA	GGACAAGTCT	AGATTCTAAC	AAGGGATTTT	201
TCCCAATTAA	TAACCAAATC	GTGTTACATC	GTATTCAACC	CAACTCCGCC	151
AAGAAAACAA	CAGTTTTTAC	TGAAATGGTG	TCGACCAAAA	CAATTTAACA	1101
TAATTGGAAA	ACGCTATCAT	AACAGTGTTG	CATTATCCGC	GTAATAAAAC	1051
AAGAAAACAA	CAGTTTTTAC	TGAÀATGGTG	TCGACCAAAA	CAATTTAACA	1001
TAGCAAGCGG	CAATCTGTTT	ATCTATTCCA	TAGGTGTAAC	TTACTATCTT	951
TTCCGCTATG	TAAAGCCACT	CACTTAGCGT	GAAAGTGCGT	CTGCTCGCAT	901
AGCGAAAAAC	AGAAAAAGGC	ACCATTCCAC	CGGGGTTGTG	TGAATTGGCA	851
TTGCTGTGTC	AATGCTTTGG	CAAACGCCTG	TCAAATTCAG	ATATATCGTC	801

FIG.7C

-			4	_			35/									
GGTAAACTTT	TCTTTCCGCC	AAAATCAGCA	ACATTAAAAA	AACTTACCTT	TAGCAAAGAA	AAAGAAAAG	CGGCAATATT	TTGTGGAGAC	AAAACAAAAG	AGACCCCCTŢ	CCGGTGAAGC	ACCAATACAA	AACGGCATCA	ACTCCCACTT	ATTGATGGAG	CGGATGGGTT
TCGAAACCAA	GCAATATTGT	ATTTCCGCTC	CGATAAAGTC			TGTATCAGGC	CGTTAATTGA	ACCGGTGGTT	TGCAATTGTT	TTGAAGCCGA						TTTATTCTGG (
CTGCCACTAT	GATAAAAGCG	TGGCGGTGTA	TGATTACAGG	TCAGGTAAAG	AGGTAAAAAC	CAACCATCAA	GGCGATATTG	TATCGCTAAA	TTGACAGCAA	GATGTAACAA	TGATGAATTC	GCGAACTCAA	AACGCCTGGA	CTCAATCAAC	AGCGTGGCGG	
AATGTCCGTG	TGTAAGCAAA	AAGCGGAAAT	GGCAAGCTGA	TATCGACCTT	AGCGCGGCGA	GAAAAAGGCT	TATTGTGTGG	GTAGTGGTGA	TATTTATCCA	AGACCCTGAT	CCGGTATAAA	AAAAAAATA	TTATCTGAAA	CCGTTAATAG	AGTAAAGGTC	TAAAGGCGGA AATTTAACCA
CGGTAACATT	CTGCTGATTC	AAAGAGGGTG	AGCTAAAGGC	CAGGTGCAGT	GGCGGTGACG	AACCTCTTTA	GCGGACGCGC	AACGCTCAAG	ATCGGGGCAT	AGTGGTTGCT	CGCAATAATA	AAGCGACCCT	CTATTTCAAA	AGAAAACTTA	AATTCTCCAT	ATATTACTTC
1601	1651	1701	1751	1801	1851	1901	1951	2001	2051	2101	2151	2201	2251	2301	2351	2401

FIG.7D.

						36	5/82								
ATATTACCGC							AGCAATAGCA	TTTTAACGGC	AAGTTAAPT	TTACCAATTC	TTTTTTGAT	ТСАСТСАААТ	GTTCGCGGCG	AACCAATTCA	GGTACGCACG
GGTTTTTAA			GGAACGGGTA	CAATCTTAGT		AACGTCAGTG	ATACATTTCA	CAGGGGTGAA		AAGCAAACCT	GGGCTCTGT	GAGTTAAAAA	AAATTCCCAT	CCATAAATGC	TTTTATGACG
AAAATATTAC GCTTGATCAG	GTGGAAATAA	GGCACTGTAA	ATCTTTAAAC	ATTTAACCCA	ATTAACCAAA	TTCGCACTGG	CCTTTATTAA	AGAAGCTCTG	CAATCTCAAA	ACATGAACAC	GCCACTGGTG	CAGAGGGGCT	ATTTACCTT	AAAGACTTAA	GAAAGATGAT
	GCTTTTGAAG	TGTCGCCCAG	CTAACAACGT	TCAGTGAATA	GAATATAACA	CCÁGCCATGA	GCAAATTTTA	AACACAGTAT	ACATGTCATT	CCAAACGAGA	CAATATCACA	ACCATTCTGG	AACGGCGCTA	TAAAATCAAC	TCAGACAGAC GAAAGATGAT
GATGTTCATA	CGCTTCCGTA	ATGCTAAAAT	GATTTCAGGG	TATCATTTCA	ACATATCTGG	TATTGGCAAA	AGAGACAGGC	AAGGCTTAAC	GTAAATGGCA	CAAATTAAAA	GGTTTTAGC	ATATATGCCA	TAATATCTCT	ATGACGCTTT	AATTTCAGCC
2451	2501	2551	2601	2651	2701	2751	2801	2851	2901	2951	3001	3051	101	151	201

FIG.7E.

37/82 GGTAATGTCA TATTACTATC CTAATCAGCA GTTAATGGGA TCTCACTATT TAAATATCAC ACACAAGGAG CATTACCACT TAATCAACAA GAAATCCAAA TTCTTCCGAT TTGATGGAGA ATTAAAACCA CAATAAAGCA ACAGTAATGA AATGTTAAAG CATTCTGGGC AATAACGCCC CAGCTTGCTC TTACGGGGAA TTAAAGGCAA AGGAAAGACT AGAGATACCC AATTAATATA GTGATTTAAA GGCGGAGATA TAATGATGCT ACCTCACGAT AAAAAGGGTA CAACCTAACT ACTATTGGCA AACTTTTAAC TTTCAGGTTT CAATGCCATC AATTCAACCT ACAACATATC GCTAGAAGCC AGCAGCAGCA TAAAACTTGG AATGCAGATA GCACTGCCGA TATCTCGCAA AAAGAAGGCA ACCAATGATG AAGCATCATC CAGACAGTAA GATAACAATC CAAGTAATGC TAGAGATTTA GACCTAAGTA CCAAAACAGT ACAAAACTCA AACTGGCGAA CAAATGTTAC CCACTTTTAA GATAGAGTTA TGGCAATGTT CGGCAATTTT ACCAATAATG GCAACCAAAG TTAAATATTA TCACCAAACA TCAGATGCGA ATTGACAGAA CCAAAGATGG GGTGCCGAAG GAGAAAGCAG CCCTTGGTGG AAACATAAGG GTTTAAGTTT TCAGAAAGCG TGGTAAAACT CACGCTAAAC AAAAGGAAGC TTGGCGGCAA GGACTCTAGT AAAATTAATA AAGAATTGAA CGGTAACAGC GAGATTACAG 3251 3301 3351 3401 3451 501 3651 551 3601 3701 3751 801 851 3901 951 4001

FIG.7F

-	D .	, -	-					8/82									
CEC K K K C C A C L				A)	CAACCAAAAC				GTTGGGAA'FG	CGCAACAGGG	CTAACCTO	ATTA ATCOTO		50105550 66ECCEACAA			CGAAAGATGG
TGACACTAAA								# O & & E E & C C	WOWY I I UDO	CAACCTTAAC	ATCACTTCAA	CGCAGGAAGC	TAACCACCGT				
GGTCACAATG					TTTCCGGTAA	TCCGGCTCAA	AACAGGTACA			GAAGGAGCTG	CGGTTCTAGC	ATGGTAGCAT	ACAGGCACCT	CACCTTGGTT	GTGATAGTAC	ACTGCGGCAA	
CTCTGCTGAC	. GCAGCAATGG	ATTACTGCAA	AGTAAATATC	TTAACGCAAC	AGCGGTACGA	AACCACTAAA	TAACAAGTGC		() () () () () ()	TAATIGCGACA	CTACTGAAGC	TTGGCTCAGA	ATTAAATACT	CAACCAGCGG	GATGCATCAG	TGGTAGTGTG	TAAACACAGT
ATTCAAAAAT	AAAACATCTA	CGGCTTAACT	CTCTCAAAAC	GGCTCGACCA	AGGTGATATC	CTGGTGATTT	GAGGCTAATG	TAATACGGTA	E K K K K K K K K K K K K K K K K K K K	GCGCAGAAAT.	AATACCTTGA	GGTAGACCTC	CTAATGTGAC	GATATTAAAG	GCTAAATGGT	ACTGGGGATT	ACTGGGGATT
4051	4101.	4151	4201	4251	4301	4351	4401	4451	4501	H O	4551	4601	4651	4701	4751	4801	4851

FIG.7G.

						3	39/82	2					,		
АААТАТАТСС			ATTACTOCI			GTAGATTTCA	GTGGGTTAAA	GAATACAATA	GCAGATTAAA	TCATTGTATG	TGCACTTGAA	ТАТСТАААТА	CTTGAATTAC	GATATTGCCG	TCTCGAAATC
AATTGAGGTG						AATTGACAAG	TATTTACTGT	ATCTTGTAAA AAATTACGGA	AATATAAAA	GGCTTCTTCA	AGTTATCTGG	GCAAAATCTT	AACAGCACAG	AATTTGATGT	TTTGAGCTAG
GAGGCAAGGA	GAAGAAGTAA	TGATGAAGAA	TTGTTGAGCC	ACCAGACCGT	AAGTGGTAAT	CGTAGTCAGT	ATTTTCGTAT	ATCTTGTAAA	TATTATGAAA	TGCTTGGCCT	AAAGGCTTTC	ACTGTCTGTA	CAAACCTAAA	GAGCCAAATA	CAATATCATG
GTGCGCTTAA	AGCAAGTGTA	AAGATTTATC	GCTGTACGTT	TGAATTTACA	CGTGTTTCTC	GATGGACAGC	AAGTCATTTT	GGCTTTACCC	AACAGGTTAT	ATATCAGTAT	GTTTTTAGTA	AAGACGCCCA	CAAACTTTAA	AGATAAGATT	TTACGGATGG CAATATCATG
TAGAAACACT	AGCCAGGTGT	GAAAAAGTAA	TGGTGTAAGT	ATACACAAAA	GAAGGTAAGG	TGTTGCTGAC	TCCTGCAATG	GTTCAGTACG	AAGTATTTT	ACTCAGTGCA	CAGAAGAAGC	ACTTTAAGTG	CCAAGGCTCG	AGGCTGTGCT	CAACAAACCA
4901	4951	5001	5051	5101	5151	5201	5251	5301	5351	5401	5451	5501	5551	5601	5651

FIG.7H.

		_					40	/82								
TATACTCA		##91010101011 ****************************				CATCTCTTAN							TOTTTHEATH.		TAGCAGTOA	GATTTATTCT
GAGCCAGGGT					GAGTTTAACT	TGGTCATGAT	TGATATCGAC	AATCTATCTC	CTTGGCATGG	TATTAATCO			ATTACCAGG			
TTTATAAGGC	CCATCTTTGA	TTTGCGTGAA	TACATTACGA	GGCTTCTCGC	CGGCGCGAGA	CCAATTTAAC	CTGATTCTAA	TCAAAAGGTC	AACATTTAAC	ACTACCGCCA	AAGAAAAAT	CCAATTTACC	ACGCGAGTAA	TTTAATCGCA	GTTTGCTCAA	TACAAGATAT
AGCCAAGTTT	TCGTAGCCTG	AGTGGTTCGA	GTTACCCGTG	GATAATTGCG	ATGATAATTT	TTTGTTAATG	ATGAGTTATG	TCGTAAATTA	ATTATCTCCC	TTAGGCTACA	GGGTGAAACG	ATGGACATAT	CATCATTATT	TGGCGAAACA	TGAGTCAAGA	CAATTTACTC
AGCCGCAGAA	AAAATATCGC	GATGGTCGTC	CCCGCTTAAG	CCTCTAATTT	TTTATTTCTT	AAGCTTGGGT	TTATACCAGT	GTGCGATTAA	AAATGGAGTT	TAAAATTAAT	TAAATCGCTT	GCAGGCATTG	TGATTTAACT	TGGAGCGCAT	AGTTTAGGGT	ATTATCAGGT
5701	5751	5801	5851	5901	5951	6001	6151	6201	6251	6301	6351	6401	6451	6501	6551	6601

FIG.7I

	GACGCTAATT	GGAAAAATG GACGCTAATT	TGGTGATTCT	CGTGAATTAA	GTTTGCTTGT	7401
	AAGATTATGA	ATCGCAAAAA	GGAACAACAT	TATTACGCTT	AAGCCCAGCC	7351
•	ACAACCACGC	GAATATTTAA	ACTCCCCTGC	CAACAATCAA	CGGAATTAAG	7301
	GCTTTACTTG	AGATGCGACC	ACGCTCCTCA	AATTTGCAAA	GACAAAAGAA	251
	TTAATAATAT	TACAAGGGAT	GCCATGGCGA	TATACTCCAT	TAAACTAAAG	7201
	ATTTATATGA	TAAAAAAACA	CAAGTAATAC	TCAAGCAAGC	CCAAGCAAAC	7151
	GCTAAGCAAA	GCTAAGCTGA	AAATAAACAA	CTTATATATC	TGTTTTTACC	7101
	TAGGCAACCC	TTACAGTCTA	ACCCGCCAAT	TATATGCTTT	AGTTTATAAC	7051
O	TCCGCCTACC	TGGTAAGCGT	TTTAATCAAC	AACCCTGAAA	TTCAGTTTCT	7001
,	GAGATTAACA	CCTTCTGGGG	TCACCTACAA	ACGCACAAGC	GCAACAAAAA	5951
	AATTTGAATG	CAATAGTGAC	TTGCAAATGC	GCTCGTCGCT	TGCTTTTGTT	5901
	TAAGCCTAGA	ACACAAAACT	AACCTCTCCT	TAGGCATTAA	TCTGCGGGTT	5851
	CACGGTATCC	AAGATATGCA	ACTTACGGCG	AAATGCTAAA	ATAATAGCGA	801
	CAGTTCCGTT	TGATGCAGGT	ATGCGTTTTA	ATCAGCCCTT	CCGCTTCCAA	6751
	CAAAATACAC	TTAAGTATGC	GCGTAATGAA	GTCTTGTATG	GGTGAGCGCG	6701
	CGGTGCAAGT	TTAAATACGG	GTCAGAGGCT	TACTTATGGC	CTGTAACAGG	651

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FIG.7J

7451	TTGGAGGCGT	TCACGATATT	GAATTTGACG	CACCCGCTCA	GCTGGCATAT	
7501	CTACCCGAAA	AATTACTAAT	TTATTTTGCC	ACTCGTCTCG	CTAATGCAAT	
7551	TACAACACTC	TTTCCGACC	CCGAATTGGC	AATTTCTGAA	GAAGGGGCGT	
7601	TAAAGATGAT	TAGCCTGCAA	CGCTGGTTGA	CGCTGATTTT	TGCCTCTTCC	
7651	CCCTACGTTA	ACGCAGACCA	TATTCTCAAT	AAATATAATA	TCAACCCAGA	
7701	TTCCGAAGGT	GGCTTTCATT	TAGCAACAGA	CAACTCTTCT	ATTGCTAAAT	
7751	TCTGTATTTT	TTACTTACCC	GAATCCAATG	TCAATATGAG		
7801	TTATGGGCAG	GGAATCAACA	ACTTTGTGCT	TCATTGTGTT	2/82 YOULDCOLL	
7851	GTCTTCACGT	TTTATTGGTA	CCGCATCTGC	GTTTCATAAA	AGAGCGGTGG	
7901	TTTACAGTG	GTTTCCTAAA	AAACTCGCCG	AAATTGCTAA	TTTAGATGAA	
7951	TTGCCTGCAA	ATATCCTTCA	TGATGTATAT	ATGCACTGCA	GTTATGATTT	
8001	AGCAAAAAAC	AAGCACGATG	TTAAGCGTCC	ATTAAACGAA	CTTGTCCGCA	
8051	AGCATATCCT	CACGCAAGGA	TGGCAAGACC	GCTACCTTTA	CACCTTAGGT	
8101	AAAAAGGACG	GCAAACĊTGT	GATGATGGTA	CTGCTTGAAC	ATTTTAATTC	
8151	GGGACATTCG	ATTTATCGTA	CACATTCAAC	TTCAATGATT	GCTGCTCGAG	
8201	AAAAATTCTA	TTTAGTCGGC	TTAGGCCATG	AGGGCGTTGA	TAAAATAGGT	

FIG.7K.

ATATAATGGA CCCGCAGTGT TGTGAGCAAC CTGCCACTAC TATGTGGGCA AGATGCCCTA ATGTACTCAG ACAATGAAAT TAAAGCTAAA GATGCCACTG GCTTGACACA GCGTGATTGC GCATAATTGA GATGAAGTAC ACCAGAATGG TGCGTCTAGC ATAGAAAACA AGTAGCAATA AACTTTCCAA CCACGATTTT CTGGGTCATC GCTTACCCAA AGAAGATGAT AAAGTGGATT TGCCGCTACC AAATCAGAGA CAATCAACAG TTTAGGTGAC TGGCAATATT GCTTAGGACT AATACTAACG CAAAACGGGG GAATGTGCTT TCGTTACATC CTTTGAAATC AACAGTGCGA CGCCCCACAA ATGGATATTA AGCTGTAGCC ATGTCATCGT ACCCTTTTAC ACATTGCAAG ATATCGGTAT CGCACTTGGA CACGATTATC TCGAAAGCTA TCCTTTCGGT TTGGTGTATG CTGTTTAAAC AACATATATT TTGAACTCCG TTGACGAGTT TTTATCCGTA CCCCTATTCA TTTATTGATT AAGCATTGGC TTTCAGCGAA GAAGTAGTCA CTTCTGCACT ATTTTGCTA ATTTTCATTT AAATGGTTTA CGCACCTTAT TTAGGTTTAG ACACACGAGA TAAATCCGTT TGATGAAGGT CAAGAACGCC CGAGAAGTGT TCTATATGCC ACTCGGCTTG GAGACTGTTT GCATTCTGAA GTGAAGATTG GGAAAACCCT TAAACCCTGA CCTTATGTAC CCCTTATGTC CACATCCCCA GTCAAAATAC GATATGCTAC TATGGTTACA ATGAACATAT CTGATAGCCG AGAAAACCAT 8251 8301 8351 8401 8451 8501 551 8651 8701 601 8751 8801 8851 8901 8951 9001 9051 ∞

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FIG.7L.

ACGGCTTACA AAAGCTTTTT ACAGGCGACC CTCGTCCATT GGGCAAAATA GTAAAAAATA TTTTAAAAAC TTTTATCTTT ATAACGATCC CGCACGCTGA GCGGAGATTT TTGCACCACA TGCGGTTAAT TTTCAAAGCG AAGCACTTGA TAAAGGCTAA AATCACCAAA GCCTTTCATG ATGGAAGCGG CAGTTTATCA GCCTCCCGCC ATAAAACTCC TACCCACAAA AAA CTGCTTAAGA AAACAAATGA TCAACCGCAC AAAGTAAAAG TGGCAGAAAT ACGGTTTTTT CTCTCAAAAA TAGCCAAAAC AAATCACCAA 9101 9151 9201 9301 9251 9351 9401

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FIG.8A

1 ATGAACAAGA TATATCGTCT CAAATTCAGC AAACGCCTGA ATGCTTTGGT

TOCTGTGTCT GAATTGACAC GGGGTTGTGA CCATTCCACA GAAAAGGCA

101 GTGAAAACC TGTTCGTACG AAAGTACGCC ACTTGGCGTT AAAGCCACTT

TCCGCTATAT TGCTATCTTT GGCCATGCCA TCCATTCCGC AATCTGTTTT

201 AGCGAGCGGT TTACAGGGAA TGAGCGTCGT ACACGGTACA GCAACCATGC

AAGTAGACGG CAATAAAACC ACTATCCGTA ATAGCGTCAA TGCTATCATC

301 AATTIGGAAAC, AATTITAACAT TGACCAAAAT GAAATGGTGC AGTTTTTACA

AGAAAGCAGC AACTCTGCCG TTTTCAACCG TGTTACATCT GACCAAATCT

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401 CCCAATTAAA AGGCATTTTA GATTCTAACG GACAAGTCTT TTTAATCAAC

CCAAATGGTA TCACAATAGG TAAAGACGCA ATTATTAACA CTAATGGCTT

501 TACTGCTTCT ACGCTAGACA TITICTAACCA AAACATCAAG GCGCGTAATT

TCACCCTTGA GCAAACCAAG GATAAAGCAC TCGCTGAAAT CGTGAATCAC

601 GGTTTAATTA CCGTTGGTAA AGACGGTAGC GTAAACCTTA TTGGTGGCAA

AGTGAAAAAC GAGGGCGTGA TTAGCGTAAA TGGCGGTAGT ATTITCTITTAC

701 TTGCAGGGCA AAAAATCACC ATCAGCGATA TAATAAATCC AACCATCACT

TACAGCATTG CTGCACCTGA AAACGAAGCG ATCAATCTGG GCGATATTTT

FIG 8B

801 TGCCAAAGGT GGTAACATTA ATGTCCGCGC TGCCACTATT CGCAATAAAG

GTAAACTTTC TGCCGACTCT GTAAGCAAAG ATAAAAGTGG TAACATTGTT

901 CTCTCTGCCA AAGAAGGTGA AGCGGAAATT GGCGGTGTAA TTTCCGCTCA

AAATCAGCAA GCCAAAGGTG GTAAGTTGAT GATTACAGGC GATAAAGTTA

1001 CATTGAAAAC GGGTGCAGTT ATCGACCTTT CGGGTAAAGA AGGGGGAAAA

ACTIVATICITIG GCGGTGACGA GCGTGAGAAA GGTAAAAACG GCATTICAATT

1101 AGCAAAGAAA ACCACTTTAG AAAAAGGCTC AACAATTAAT GTGTCAGGTA

AAGAAAAAGG TGGGCGCGCT ATTGTATGGG GCGATATTGC GTTAATTGAC

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1201 GGCAATATTA ATGCCCAAGG TAAAGATATC GCTAAAACTG GTGGTTTTGT

GGAGACGTCG GGGCATTACT TATCCATTGA TGATAACGCA ATTGTTAAAA

1301 CAAAAGAATG GCTACTAGAC CCAGAGAATG TGACTATTGA AGCTCCTTCC

GCTTCTCGCG TCGAGCTGGG TGCCGATAGG AATTCCCACT CGGCAGAGGT

1401 GATAAAAGTG ACCCTAAAAA AAAATAACAC CTCCTTGACA ACACTAACCA

ATACAACCAT ITCAAATCIT CICAAAAGIG CCCACGIGGI GAACATAACG

1501 GCAAGGAGAA AACTTACCGT TAATAGCTCT ATCAGTATAG AAAGAGGCTC

CCACTTAATT CICCACAGIG AAGGICAGGG CGGICAAGGI GIICAGAITG

FIG.8C

1601 ATAAAGATAT TACTTCTGAA GGCGGAAATT TAACCATTTA TTCTGGCGGA

TGGGTTGATG TTCATAAAAA TATTACGCTT GGTAGCGGCT TTTTAAACAT

1701 CACAACTAAA GAAGGAGATA TCGCCTTCGA AGACAAGTCT GGACGGAACA

1801 ITTAGAITTA ACAACGICIC ICTAAACAGC CITGGCGGAA AGCIGAGCIT

ACCTAACCAT TACAGCCCAA GGGACCATCA CCTCAGGTAA TAGTAACGC

TACTGACAGC AGAGGGACA GAGGTAGAAG AACTAAGGGT AATATCTQAA

1901 ACAAATITGA CGGAACGITA AACATITCCG GAACTGTAGA TATCTCAATG

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AAAGCACCCA AAGTCAGCTG GTTTTACAGA GACAAAGGAC GCACCTACTG

2001 GAACGTAACC ACTITTAAATG ITTACCTCGGG TAGTAAATTT AACCTCTCCA

ITGACAGCAC AGGAAGTGGC TCAACAGGTC CAAGCATACG CAATGCAGAA

2101 TTAAATGGCA TAACATTTAA TAAAGCCACT TTTAATATCG CACAAGGCTC

AACAGCTAAC TTTAGCATCA AGGCATCAAT AATGCCCTTT AACAGTAACG

2201 CTAACTACGC ATTATTTAAT GAAGATATTT CAGTCTCAGG GGGGGGTAGC

CITAATITICA AACITAACGC CICATCIAGC AACATACAAA CCCCIGGCGI

3301 AATTATAAAA TCTCAAAACT TTAATGTCTC AGGAGGGTCA ACTTTAAATC

TCAAGGCTGA AGGTTCAACA GAAACCGCTT TTTCAATAGA AAATCATTTA

FIG.8D

2401 AACTTAAACG CCACCGGTGG CAATATAACA ATCAGACAAG TCGAGGGTAC

CGAITICACGC GICAAAAG GIGICGCAGC CAAAAAAAA ATAACITITIA

2501 AAGGGGGTAA TATCACCTTC GGCTCTCAAA AAGCCACAAC AGAAATCAAA

GCCAATGTTA CCATCAATAA AAACACTAAC GCTACTCTTT GTGGTGCGAA

2601 TITIGCCGAA AACAAAICGC CTITAAATAT AGCAGGAAAT GITAITAATA

ATGGCAACCT TACCACTGCC GGCTCCATTA TCAATATAGC CGGAAATCTT

2701 ACTGTTTCAA AAGGCGCTAA CCTTCAAGCT ATAACAAATT ACACTTTTAA

TGTAGCCOGC TCATTTGACA ACAATGGCGC TTCAAACATT TCCATTGCCA

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2801 GAGGAGGGC TAAATTTAAA GATATCAATA ACACCAGTAG CTTAAATATT

ACCACCAACT CTGATACCAC TTACCGCACC ATTATAAAAG GCAATATATC

2901 CAACAAATCA GGTGATTTGA ATATTATTGA TAAAAAAAGC GACGCTGAAA

TCCAAATTGG CGGCAATATC TCACAAAAAG AAGGCAATCT CACAATTTCT

3001 TCTGATAAAG TAAATATTAC CAATCAGATA ACAATCAAAG CAGGCGTTGA

AGGGGGCGT TCTGATTCAA GTGAGGCAGA AAATGCTAAC CTAACTATTC

3101 AAACCAAAGA GTTAAAATTG GCAGGAGACC TAAATATTTC AGGCTTTAAT

AAAGCAGAAA TTACAGCTAA AAATGGCAGT GATTTAACTA TTGGCAATGC

FIG.8E

3201 TAGCCGTGGT AATGCTGATG CTAAAAAGT GACTTTTGAC AAGGTTAAAG

ATTCAAAAAT CTCGACTGAC GGTCACAATG TAACACTAAA TAGGGAAGTG

3301 AAAACGICTA AIGGIAGIAG CAAIGCIGGI AAIGATAACA GCACCGGITT

AACCATTITCC GCAAAGATG TAACGGTAAA CAATAACGTT ACCTCCCACA

3401 AGACAATAAA TATCTCTGCC GCAGCAGGAA ATGTAACAAC CAAAGAAGGC

ACAACTATCA ATGCAACCAC AGGCAGGGTG GAAGTAACTG CTCAAAATGG

3501 TACAATTAAA GGCAACATTA CCTCGCAAAA TGTAACAGTG ACAGCAACAG

AAAATCITGI TACCACAGAG AATGCTGTCA TTAATGCAAC CAGCGGCACA

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3601 GTAAACATTA GTACAAAAC AGGGGATATT AAAGGTGGAA TTGAATCAAC

TICCGGTAAT GTAAATATTA CAGCGAGCGG CAATACACTT AAGGTAAGTA

3701 ATATCACTGG TCAAGATGTA ACAGTAACAG CGGATGCAGG AGCCTTGACA

ACTACAGCAG GCTCAACCAT TAGTGCGACA ACAGGCAATG CAAATATTAC

3801 AACCAAAACA GGTGATATCA ACGGTAAAGT TGAATCCAGC TCCGGCTCTG

TAACACITIGT IGCAACTIGGA GCAACTCITIG CIGTAGGTAA TAITITCAGGT

3901 AACACTGTTA CTATTACTGC GGATAGCGGT AAATTAACCT CCACAGTAGG

TICTACAATT AATGGGACTA ATAGTGTAAC CACCTCAAGC CAATCAGGGG

FIG.8F

4001 ATATTGAAGG TACAATTTCT GGPAATACAG TAAATGTTAC AGCAAGCACT

GGTGATITIAA CTATTGGAAA TAGTGCAAAA GTTGAAGCGA AAAATGGAGC

1101 TGCAACCTTA ACTGCTGAAT CAGGCAAATT AACCACCCAA ACAGGCTCTA

GCATTACCTC AAGCAATGGT CAGACAACTC TTACAGCCAA GGATAGCAGT

1201 ATCGCAGGAA ACATTAATGC TGCTAATGTG ACGTTAAATA CCACAGGCAC

TTTAACTACT ACAGGGGATT CAAAGATTAA CGCAACCAGT GGTACCTTAA

301 CAATCAATGC AAAAGATGCC AAATTAGATG GTGCTGCATC AGGTGACCGC

ACAGTAGTAA ATGCAACTAA CGCAAGTGGC TCTGGTAACG TCACTGCCAA 60 88

401 AACCTCAAGC AGCGTGAATA TCACCGGGGA TTTAAACACA ATAAATGGGT

TAAATATCAT ITCGGAAAAT GGTAGAAACA CIGTGCGCTT AAGAGGCAAG

501 GAAATTGATG TGAAATATAT CCAACCAGGT GTAGCAAGCG TAGAAGAGGT

AATTGAAGCG AAACGCGTCC TTGAGAAGGT AAAAGATTTA TCTCATCAAG

iol aaagagaaac actagccaaa cttggtgtaa gtgctgtacg tttcgttgag

CCAAATAATG CCATTACGGT TAATACACAA AACGAGTTTA CAACCAAA.CC

'01 ATCAAGTCAA GTGACAATTT CTGAAGGTAA GGCGÌGTTTC TCAAGTGGTA

ATGCCCACC ACTATGTACC AATGTTGCTG ACGATGGACA GCAG

FIG.9A

1 ATGAACAAGA TATATCGTCT CAAATTCAGC AAACGCCTGA ATGCTTTGGT

TECTGTGTCT GAATTGACAC GGGGTTGTGA CCATTCCACA GAAAAGGCA

101 GTGAAAAACC TGTTCGTACG AAAGTACGCC ACTTGGCGTT AAAGCCACTT

TCCGCTATAT TGCTATCTTT GGGCATGGCA TCCATTCCGC AATCTGTTTT

201 AGCGAGCGGT TTACAGGGAA TGAGCGTCGT ACACGGTACA GCAACCATGC

AAGTAGACGG CAATAAAACC ACTATCCGTA ATAGCGTCAA TGCTATCATC

301 AATTGGAAAC AATTTAACAT TGACCAAAAT GAAATGGTGC AGTTTTTACA

AGAAAGCAGC AACTCTGCCG TTTTCAACCG TGTTACATCT GACCAAATCT &

401 CCCAATTAAA AGGGATTTTA GATTCTAACG GACAAGTCTT TTTAATCAAC

CCAAATGGTA TCACAATAGG TAAAGACGCA ATTATTAACA CTAATGGCTT

501 TACTGCTTCT ACGCTAGACA TITICTAACGA AAACATCAAG GCGCGTAATT

TCACCCTTGA GCAAACCAAG GATAAAGCAC TCGCTGAAAT CGTGAATCAC

601 GGITTIAATTA CCGTTGGTAA AGACGGTAGC GTAAACCTTA TTGGTGGCAA

AGTGAAAAAC GAGGGCGTGA TTAGCGTAAA TGGCGGTAGT ATTTCTTTAC

701 TTGCAGGGCA AAAAATCACC ATCAGCGATA TAATAAATCC AACCATCACT

TACAGCATTG CTGCACCTGA AAACGAAGCG ATCAATCTGG GCGATATTTT

FIG.9B

801 TGCCAAAGGT GGTAACATTA ATGTCCGCGC TGCCACTATT CGCAATAAAG

GTAAACTTTC TGCCGACTCT GTAAGCAAAG ATAAAAGTGG TAACATTGTT

901 CTCTCTGCCA AAGAAGGTGA AGCGGAAATT GGCGGTGTAA TTTCCGCTCA

AAATCAGCAA GCCAAAGGTG GTAAGTTGAT GATTACAGGT GATALAGTCA

1001 CATTAAAAAC AGGTGCAGTT ATCCACCTTT CAGGTAAAGA AGGGGGAGAG

ACTTATCTTG GCGGTGATGA GCGTGGCGAA GGTAAAAATG GTATTCAATT

TAAT GTATCAGGCA AAGAAAAAGG CGGGCGCGCT ATTGTATGGG GCGATAITGC ATTAATTAAT **S** 1101 AGCGAAGAAA ACCTCTTTAG AAAAAGGCTC GACAATTAAT GTATCAGGCA

1201 GGTAACATTA ATGCTCAAGG TAGCGATATT GCTAAAACTG GCGGCTTTGT

GGAAACATCA GGACATGACT TATCCATTGG TGATGATGTG ATTGTTGACG

1301 CTAAAGAGTG GTTATTAGAC CCAGATGATG TGTCCATTGA AACTCTTACA

TCTGGACGCA ATAATACCGG CGAAAACCAA GGATATACAA CAGGAGATGG

401 GACTAAAGAG TCACCTAAAG GTAATAGTAT TTCTAAACCT ACATTAACAA

ACTCAACTOT TGAGCAAATC CTAAGAAGAG GTTCTTATGT TAATATCACT

501 GCTAATAATA GAATTTATGT TAATAGCTCC ATCAACTTAT CTAATGGCAG

TITIAACACIT CACACTAAAC GAGATGGAGT TAAAATTAAC GGTGATATTA

FIG.9C

1601 CCTCAAACGA AAATGGTAAF TTAACCATTA AAGCAGGCTC TTGGGTTGAF

GITCATAAAA ACAICACGCT IGGIACGGGT ITITIGAATA ITGICGCIGG

1701 GGAITCIGTA GCTTTTGAGA GAGAGGGGGA TAAAGCACGT AACGCAACAG

ATGCTCAAAT TACCGCACAA GGGACGATAA CCGTCAATAA AGATGATAAA

1801 CAATTTAGAT TCAATAATGT ATCTATTAAC GGGACGGGCA AGGGTTTAAA

GITTATTIGCA AATCAAAATA ATTITCACTCA TAAATTTIGAT GGCGAAATTA

1901 ACATATCTGG AATAGTAACA ATTAACCAAA CCACGAAAAA AGATGTTAAA

TACTGGAATG CATCAAAAGA CTCTTACTGG AATGTTTCTT CTCTTACTTT & 8

2001 GAATACGGTG CAAAAATTTA CCTTTATAAA ATTCGTTGAT AGCGGCTCAA

ATTCCCAAGA TTTGAGGTCA TCACGTAGAA GTTTTGCAGG CGTACAITTT

101 AACGGCATCG GAGGCAAAAC AAACTTCAAC ATCGGAGCTA ACGCAAAAGC

CTTATITIAAA TIAAAACCAA ACGCCGCTAC AGACCCAAAA AAAGAATTAC

201 CTAITACTTT TAACGCCAAC ATTACAGCTA CCGGTAACAG TGATAGCTCT

GIGAIGITIG ACATACACGC CAATCTTACC ICTAGAGCTG CCGGCATAAA

301 CATGGATTCA ATTAACATTA CCGGCGGCT TGACTTTTCC ATAACATCCC

ATAATCGCAA TAGTAATGCT TITGAAATCA AAAAAGACTT AACTPIAAAT

FIG.9D

2401 GCAACTGGCT CGAATTTTAG TCTTAAGCAA ACGAAAGATT CTTTTTATAA

TGAATACAGC AAACACGCCA TTAACTCAAG TCATAATCTA ACCATTCTTG

2501 GCGGCAATGT CACTCTAGGT GGGGAAAATT CAAGCAGTAG CATTACGGGC

AATATCAATA TCACCAATAA AGCAAATGTT ACATTACAAG CTGACACCAG

2601 CAACAGCAAC ACAGGCTTGA AGAAAAGAAC TCTAACTCTT GGCAATATAT

CIGITGAGGG GAATITAAGC CTAACTGGTG CAAATGCAAA CATTGTCGGC

2701 AATCTTTCTA TTGCAGAAGA TTCCACATTT AAAGGAGAAG CCAGTGACAA

CCTAAACATC ACCGGCACCT TTACCAACAA CGGTACCGCC AACATTAATA

2801 TAAAACAAGG AGTGGTAAAA CTCCAAGGCG ATATTATCAA TAAAGGTGGT

TTAAATATCA CTACTAAGGC CTCAGGCACT CAAAAAACCA TTATTAACGG

54/82

1901 AAATATAACT AACGAAAAAG GCGACTTAAA CATCAAGAAT ATTAAAGCCG

ACGCCGAAAT CCAAATTGGC GGCAATATCT CACAAAAGA AGGCAATCTC

.001 ACAATTTCTT CTGATAAAGT AAATATTACC AATCAGATAA CAATCAAAGC

AGGOGTTGAA GGGGGGCGTT CTGATTCAAG TGAGGCAGAA AATGCTAACC

101 TAACTATTCA AACCAAAGAG TTAAAAITIGG CAGGAGACCT AAATATTTCA

GGCTITTAATA AAGCAGAAAT TACAGCTAAA AATGGCAGTG ATTTAACTAT

201 TGGCAATGCT AGCGGTGGTA ATGCTGATGC TAAAAAAGTG ACTTTTGACA

AGGTTAAAGA TTCAAAAATC TCGACTGACG GTCACAATGT AACACTAAAT

FIG.9E

3301 AGCGAAGTGA AAACGTCTAA TGGTAGCAATGCTGGTA ATGATAACAG

CACCGGITTA ACCATITICCG CAAAAGATGT AACGGTAAAC AATAACGITTA

3401 CCTCCCACAA GACAATAAAT ATCTCTGCCG CAGCAGGAAA TGTAACAACC

3501 TCAAAATGGT ACAATTAAAG GCAACATTAC CTCGCAAAAT GTAACAGTGA

AAAGAAGGCA CAACTATCAA TGCAACCACA GGCAGCGTGG AAGTAACTGC

CAGCAACAGA AAATCTTGTT ACCACAGAGA ATGCTGTCAT TAATGCAAGC

3601 AGCGGCACAG TAAACATTAG TACAAAACA GGGGATATTA AAGGTGGAAT

TGAATCAACT TCCGGTAATG TAAATATTAC AGCGAGCGGC AATACACTTA

55/82

3701 AGGTAAGTAA TATCACTGGT CAAGATGTAA CAGTAACAGC GGATGCAGGA

GCCTTGACAA CTACAGCAGG CTCAACCATT AGTGCGACAA CAGGCAATGC

801 AAATATTACA ACCAAAACAG GTGATATCAA CGGTAAAGTT GAATCCAGCT

CCGGCTCTGT AACACTTGTT GCAACTGGAG CAACTCTTGC TGTAGGTAAT

.901 ATTICAGGTA ACACTGTTAC TATTACTGCG GATAGCGGTA AATTAACCTC

CACAGTAGGT TCTACAATTA ATGGGACTAA TAGTGTAACC ACCTCAAGCC

001 AATCAGGCGA TATTGAAGGT ACAATTTCTG GTAATACAGT AAATGTTACA

GCAAGCACTG GTGATTTAAC TATTTGGAAAT AGTGCAAAAG TTGAAGCGAA

FIG.9F

4101 AAATGGAGCT GCAACCTTAA CTGCTGAATC AGGCAAATTA ACCACCCAAA

CAGGCTCTAG CATTACCTCA AGCAATGGTC AGACAACTCT TACAGCCAAG

4201 GATAGCAGTA TCGCAGGAAA CATTAATGCT GCTAATGTGA CGTTAAATAC

CACAGGCACT TTAACTACTA CAGGGATTC AAAGATTAAC GCAACCAGTG

1301 GTACCTTAAC AATCAATGCA AAAGATGCCA AATTAGATGG TGCTGCATCA

GGTGACCGCA CAGTAGTAAA TGCAACTAAC GCAAGTGGCT CTGGTAACGT

401 GACTGCGAAA ACCTCAAGCA GCGTGAATAT CACCGGGGAT TTAAACACAA

TAAATGGGTT AAATATCATT TCGGAAAATG GTAGAAACAC TGTGCCCTTA 98

501 AGAGGCAAGG AAATTGATGT GAAATATATC CAACCAGGTG TAGCAAGCGT

AGAAGAGGTA ATTGAAGCGA AACGCGTCCT TGAGAAGGTA AAACATTTAT

601 CTGATGAAGA AAGAGAAACA CTAGCCAAAC TTGGTGTAAG TGCTGTACGT

TICGTICAGC CAAATAATGC CAITTACGGIT AATACACAAA ACGAGITTAC

101 AACCAAACCA TCAAGTCAAG TGACAATTTC TGAAGGTAAG GCGTGTTTCT

CAAGTOSTAA TOGCOCACGA GTATGTACCA ATCTTGCTGA CGATOCAGG

101 CAG

FIG.10A

COMPARISON OF DERIVED AMINO ACID SEQUENCE

50 KVRHLALKPL	KVRHLALKPL	KVRHLALKPL	KVRHLALKPL 52/85	100 TIRNSWAII	TIRNSVNAII	TIRNSVNALI	TIRNSVNAII
EKGSEKPVRT	EKGSEKPVRT	EKGSEKPVRT	EKGSEKPVRT	ATMOVICANKT	ATMOVIDGINKT	ATMOVIDGINKT	ATMOVIDGINKT
ELTRGCDHST	ELTRGCDHST	ELTRGCDHST	ELTRGCDHST	LQCMSWHGT	LQCMSWHGT	LQGMSWHGT	LQGMSVVHGT
KRLNALVAVS	KRLNALVAVS	KRLNALVAVS	KRLNALVAVS	SIPQSVLASG	SIPQSVLASG	SIPQSVLASG	SIPQSVLASG
1 MNKIYRLKFS	MIKIYRLKFS	MIKIYRLKFS	MIKIYRLKFS	51 SAILLSLGMA	SAILLSLGMA	SAMLLSLGVT	SAMLLSLGVT
Hmv3com	Hrw4com	Himlcon	Hrw2com	Hmw3com	· Hmw4com	Hmw2com	Hrw2com

FIG. 10

				58	3/82				
	150 DSNSQVFLIN	DSNSQVFT_IN	DSNSQVFLIN	DSNSQVFLIN		200 DKALAEITANH	DKALAEIVNH	DKALAEIVNH	DKALAEIVNH
	DQISQLKSIL	DŽISŽIKGIT	NQISQLKGIL	NQISQLKGIL		ARNFTILEOTK	ARNFTILEQITK	ARNFTLEQTK	ARNFTLEQTK
	NSAVFNRVTS	NSAVFNRVTS	NSAVFNRVTS	NSAVFNRVTS		TLDISNENTK	TLDISNENIK	TLDISNENIK	TLDISNENIK
	EMEQFTQESS	EMEQFLQESS	EMVQFTQEINN	EMVQFTQENIN		IINIINSFTAS	IININSFTAS	IININSFTAS	IININSFTĄS
101	NWKQFNIDQN	NWKQFINIDQN	NWKQFINIDQN	NWKQFNIDQN		151 PNGITIGKDA	PNGITIGKDA	PNGITIGKDA	PNGITIGKDA
	Hrw3com	Hmw4com	Hm1com	Hmw2com		Hmw3com	Hrw4com	Hmv1com	Hmw2com

FIG. 10(

	250 ISDIINPTIT	ISDIINPTIT	ISDIINPTIT	59 LILANIIQSI	300 VSKDKSGNIV
	ISLLAGOKIT	ISLLAGOKIT	ISILAGOKIT	ISLLAGOKIT	300 RNKGKLSADS VSKDKSGNIV
	EGVISVNGGS	EGVISVNGGS	EGVISVNGGS	EGVISVINGGS	GNINVRAATI
	GLITVGKDGS VNLIGGKVKN	VNLIGGKVKN	VNLIGGKVKN	VNLIGGKVKN	INLGDIFAKG GNINVRAATI
201	GLITVGKDGS	GLITVGKDGS	GLITVGKDGS	GLITVGKDGS	251 YSIAAPENEA
	Hmv3com	Hmw4com	Hmwlcom	Hmw2com	Hmw3com

FIG. 10D.

VSKDKSGNTV	VINDUMUM:		V NECENT V
RNKGKLSADS	RNKGKI, SADS	BNKGKI CADO	CARCANDANA
GNINVRAATI	GNINVRAATI	GNINVRAATT	1
INLGDIFAKG	VNLGDIFAKG	VNLGDIFAKG	
YSIAAPENEA INLGDIFAKG GNINVRAATI RNKGKLSADS VSKDKSGNTV	YSIAAPENEA VNLGDIFAKG GNINVRAATI RNKGKI,SANS VSKNVGONIU	YSIAAPENEA VNLGDIFAKG GNINVRAATT RNKGKISAAG VGKBKGGNI	
Hmw4com	Hmw1com	Hmw2com	

TDLSGKEGGE 90/09 350 GGVISAQNQQ AKGGKLMITG DKVTLKTGAV IDLSGKEGGE IDLSGKEGGE IDLSGKEGGE DKVTLKTGAV DKVTLKTGAV DKVTLKTGAV GGVISAQNQQ AKGGKLMITG GGVISAQNQQ AKGGKLMITG GGVISAQNQQ AKGGKLMITG LSAKEGEAEI LSAKEGEAEI LSAKEGEAEI LSAKEGEAEI 301 Hmw3com Hmw4com Hmw1com Hmw2com

400 IVWGDIALID IVWGDIALID IVWGDIALID IVWGDIALID TYLGGDERGE GKNGIQLAKK TTLEKGSTIN VSGKEKGGRA VSGKEKGGRA TTLEKGSTIN VSGKEKGGRA GKNGIQLAKK TTLEKGSTIN VSGKEKGGRA TTLEKGSTIN GKNGIQLAKK GKNGIQLAKK TYLGGDERGE TYLGGDERGE TYLGGDERGE 351 Hmw3com Hmw2com Hmw4com Hmw1com

FIG. 10E

401

450 DPENVTIEAP DPDDVSIETL DPDNVTINAE DPDDVTIEAE SGHYLSIDDN AIVKTKEWLL VIVDAKEWLL AIVDAKEWLL AIVKTKEWLL SGHDLSIGDD SGHYLSIESN SGHDLFIKDN IAKTGGFVET IAKTGGFVET IAKTGGFVET IAKTGGFVET GNINAQGK.D GNINAQGSGD GNINAQGS.D GNINAQGSGD Hmw3com Hmw4com Hmw1com Hmw2com

451

61/82 500 ILRRGSYVNI SASRVELGAD RNSHSAEVIK VTLKKNNTSL TTLTNTTISN LLKSAHVVNI ILKKGTFVNI TTLTNTTISN YLKNAWTMNI PTLTNSTLEQ TTLTNTTLES ESPKGNSISK STPKRNKE.K SDPKKNSELK DEYTGSGNSA QGYTTGDGTK DEFPTGTGEA TSGRNNTGEN TAGRSNTSED DPLRNNTGIN Hmw3com Hmw4com Hmw1com Hmw2com

501

550 .E...GGNLT NE...NGNLT GDDTRGANLT · · · SKGGNLT SISIERGSHL ILHSEGQGGQ GVQIDKDITS GVKINGDITS GVEINNDITT ILHSKGQRGG GVQIDGDIT. TLHTK...RD TLWSEGRSGG SINLSNGS.L SINL. SNGSL SINGSNGSHL TARRKLTVNS TANNRIYVNS TANQRIYVNS TASRKLTVNS Hmw3com Hmw4com Hmw1com Hmw2com

· · LTHNLSGT

FIG. 10F

51

009 ..NNLTITAQ AFEREGDKAR NATDAQITAQITGQ DANNLTITAQ KNITLD.QGF LNITA.AS.V AFEGGNNKAR LNITTKEGDI AFEDKSGR.. AFEKGSNQV. LNIVAGDS.V KNISLGAQGN INITAKQD.I IYSGGWVDVH KNITLGS.GF KNITLGT.GF IKAGSWVDVH IYSGGWVDVH IYSGGWVDVH Hmw3com Hmw4com Hmw1com Hmw2com

62/82 650 GNISNKFDGT .NFTHKFDGE YAITNKFEGT GTITSG.NSN GFRFNNVSLN SLGGKLSFTD SREDRGRRTK KRTN....K NQN SVNN GTGKGLKFIA GFRFNNVSLN GTGSGLQFTT GTGKGLNIIS GTITVNKDDK QFRFNNVSIN DFRANNVSLN GTIT.SGNQK GTVTITGEGK 601 Hmw3com Hmw4com Hmw1com Hmw2com

700 LNISGTVDIS MKAPKVSWFY RD.KGRTYWN VTTLNVTSGS KFNLSIDSTG KFTF.IKFVD EFNLTIDSRG VSSLTLNTVQ LTSLNVSESG QTTKKDVKYW NA.SKDSYWN MVLPKNESGY DKFKGRTYWN INISGIVTIN LNISGKVNIS 651 Hmw3com Hmw4com Hmw1com

FIG. 10G.

NFTF. IKYIS QTSHD.SHWN VSALNLETGA QTTRKNTSYW INISGNITIN Hmw2com

701

750 NFSIKASIMP LFKLKPNAAT NFDIKAPIGI SFNLKEGAKV NFKLKPNENM ITFN....KA TFNIAQGSTA NFNIGANAKA TFNVERNARV V..N.;.GNM VHFNGIGGKT ISFN...KDT RSSAGVNFNG IRNA..ELNG LRSSRRSFAG · · · · PYNLNG SGSNS...QD SNSKGLTTQY SGSTG...PS SDSAGTLTQ. Hmw3com Hmw4com Hmw1com Hmw2com

GGSVNFKLN ASSSNIQTPG VIIKSQNFNV AGINMDSINI VVINSKYFNV AELKMSEINI A...NLTSRA .GGSVDFTLL ASSSNVQTPG .GGSVFFDIY ANHS...GRG SDSSVMFDIH FNANITATGN FNEDISVSG. FNGNISVSG. FLANITATG. DPKKELPIT. FKSNANYAL. NKYSSLNYAS NTSKPLPI.R Hmw3com Hmw4com Hmw1com Hmw2com

850 801

T. DSRVNKG SFYNEYSKHA ENDLNLNATG GNITIRQVEG SNFSLKQTKD KKDLTINATG EGSTETAFSI HNRNSNAFEI SGGSTLNLKA TGGLDFSITS Hmw3com Hmw4com

T..DGMIGKG DFYDGYARNA EKDLTLNATG GNITLLQVEG SNFSLRQTKD NKDLTINATN SGSTKTGFSI HVRGDDAFKI SNGANFTLNS STGSSLRFKT Hmw1com Hmw2com

900

VAAKKNITFK GGNITFGSQK ATTEIKGNVT INKNTNATLR GANFAEN... Hmw3com

851

ADTSNSNTGL ITNKANVTLQ SSSSITGNIN GGNVTLGGEN INSSHNLTIL Hmw4com

GSDFDNHQ. INNNANVTLI AVTEIEGNVT GGNITFGSRK IVAKKNITFE Hmw1com

ANNAPNQQNI IEKAANVTLE INSTYNISIL GGNVTLGGQN SSSSITGNIT Hmw2com

64/82

950 901

INNGNLTTAG SIINIAGNLT VSKGANLQAI TNYTFNVAGS KSPLNIAGNV Hmw3com

ASDNLNITGT IAEDSTFKGE SVEGNLSLTG ANANIVGNLS KKRTLTLGNI Hmw4com

TNFTFNVGGL VESNANFKAI INSGNLTAGG NIVNIAGNLT KPLTIKKDVI Hmw1com

TRDTLNITGN ISESATFKGK RDRVIKLGSL LVNGSLSLTG ENADIKGNLT Hmw2com

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H	4
G	4

TTNSDTTYRT IIKGNISNKS IINGNITNEK IISGNITNKN IIGGDIINNK TTHAKRNQRS TTNASGTQKT TTNSSSTYRT DINNISSINI DINNKGGLNI DIDNSKNLSI ITQGVVKLG. NVTNDGDLNI IARGGAKFK. IAKGGARFK. IKQGVVKLQG FDNNGASNIS FINNGTAEIN FDNKGNSNIS FTNNGTANIN Hmw3com Hmw4com Hmw1com Hmw2com

1050 1001

TIKAGVDGEN 99/59 SDKVNITNQI TIKAGVEGGR TIKAGVEGGR SDKINITKQI TIKKGIDGED SDKVNITNQI SDKINITKQI SQKEGNLTIS SQKEGNLTIS SQKEGNLTIS SQKEGNLTIS DAEIQIGGNI DTEMQIGGDI DAEIQIGGNI GSLNITDSNN DAEIQIGGNI GDLNIIDKKS GDLNIKNIKA GDLNITNEGS Hmw3com Hmw4com Hmw1com Hmw2com

1100 1051

DLTIGNASGG DLTIGNASGG DLTIGNTNSA DLTIGNSNDG SDSSEAENAN LTIQTKELKL AGDLNISGFN KAEITAKNGS TEDLSISGFN KAEITAKDGR KAEITAKNGS KAEITAKDGS AGDLNISGFN TQDLNISGFN LTIQTKELKL LTIKTKELKL LTIKTKELKL SDSSEAENAN SDSDATNNAN SSSDATSNAN Hmw1com Hmw3com Hmw4com Hmw2com

NGKASIT.

FIG. 10J

1101

1150 SNAGNDNSTG SNAGNDNSTG TEDSSDNNAG RESNSDNDTG EVKT..SNGS EVKT..SNGS KVETSGSNNN KVKTSSSNGG ADGHNVTLNS TDGHNVTLNS TDGHNVTLNS ADGHKVTLHS FDKVKDSKIS FNQVKDSKIS FNNVKDSKIS FDKVKDSKIS N..ADAKKVT N..ADAKKVT D.GTNAKKVT NSGAEAKKVT Hmw3com Hmw4com Hmw1com Hmw2com

66/82 1200 TGSVEVTAQN TGSVEVTAQN TGNVEIT.. TKEGTTINAT TKEGTTINAT TKTGTTINAT TTAGSTINAT LTISAKDVTV NNNVTSHKTI NISAAAGNVT SISATSGEIT NISAAAGNVT NITA.SEKVT NNNITSHKAV LTISAKDVTV NNNVTSHKTI LTITAKNVEV NKDVTSLKTV LTIDAKNVTV 1151 Hmw3com Hmw4com Hmw1com Hmw2com

1250 TGDIKGGIES TGDIKGGIES TGDIKGGIES TSGTVNISTK TSGTVNISTKAQ GTIKGNITSQ NVTVTATENL VTTENAVINA GTIKGNITSQ NVTVTATENL VTTENAVINA 1201 Hmw3com Hmw4com Hmw1com

						67/8	32						
	. 1300	ISATTGNANI	ISATTGNANI	IKG.TESVTT		1350	ADSGKLTSTV	ADSGKLTSTV	ATESLTTQSN	ATVDLTTKSG	1400	NSAKVEAKNG	NSAKVEAKNG
TK		GALTTTAGST	GALTTTAGST	GALTTLAGST			NISGNTVTIT	NISGNTVTIT	TISGGTVEVK	TISGNTVSVS		TASTGDLTIG	TASTGDLTIG
		GQDVTVTADA	GQDVTVTADA	GNTVTVTANS			VATGATLAVG	VATGATLAVG		· · · · · · · · · · · · · · · · · · ·		GTISGNTVNV	GTISGNTVNV
		GNTLKVSNIT	GNTLKVSNIT	EGALAVSNIS			VESSSGSVTL	VESSSGSVTL				TTSSQSGDIE	TTSSQSGDIE
	1251	TSGNVNÍTAS	TSGNVNITAS	SSGSVTLTAT		1301	TTKTGDINGK	TTKTGDINGK	SSQSGDIG	GDIS	1351	GSTINGTNSV	GSTINGTNSV
FIG.10K. Hmw2com		Hmw3com	Hmw4com	Hmw1com	Hmw2com		Hmw3com	Hmw4com	Hmw1com	Hmw2com		Hmw3com	Hmw4com

GTISGNTVNV TANAGDLTVG NGAEINATEG NGAEINATEG TANAGDLTVG GTISGNTVNV NVTSATGTIG NVTSATGTIG SKIKATTGEA SKIEAKSGEA Hmw1com Hmw2com

1401

68/82 1450 SSNGQTTLTA KDSSIAGNIN AANVTLNTTG AANVTLNTTG AANVTLNTTG STKGQVDLLA QNSSIAGNIN AANVTLNTTG KDSSIAGNIN QDSSVAGSIN SSNGQTTLTA SAKGQVNLSA LTTEASSHIT AATLTAESGK LTTQTGSSIT AATLTAESGK LTTQTGSSIT LTTEAGSSIT AATLTTSSGK AATLTATGNT Hmw3com Hmw4com Hmw1com Hmw2com

1451

1500 TLTTTGDSKI NATSGTLTIN AKDAKLDGAA SGDRTVVNAT NASGSGNVTA NASGSGNVTA NANGSGSVIA SGDSTEVNAV NASGSGSVTA LGNHTVVNAT SGDRTVVNAT AKDAKLDGAA AKDAELNGAA AKDAKLNGDA NATSGTLTIN NATSGTLTIN KATSGTLTIN TLTTGDSKI TLTTVKGSNI TLTTVAGSDI Hmw3com Hmw4com Hmw1com Hmw2com

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	IQPGVASVEE	IQPGVASVEE	· (IQPGIASVDE	IQPGVASVEE
1 0 0 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0	TOPGVASVEE	ISENGKNTVR LRGKEIDVKY IQPGVASVEE	T.KCIVT TATI	TOTAL TOPGIASVDE	ISKUGRNTVR LRGKEIEVKY IQPGVASVEE
ISENGRNAVE		LOENGRIN'I'VR	ISKNGINTVI	F	1 S K DG KNTVR
DLNTINGLNI	DLNTTNCLNT	T NTT O NT H I	DLITINGLNI	DI,NTMACT NIT	
KTSSSVNITG	KTSSSVNITG	の 日 日 日 日 日 日 日 日 日 日 日 日 日 日 日 日 日 日 日	STINARCTT	ATSSSVNITG	,
Hmw3com	Hmw4com	Hmw1com		Hmw2com	

1600	. VILLANDEEKE TLAKLGVSAV RFVEPNNAIT VNTQNEFTTK	ONNATT TIMESTER	JEK VKDI,SDRFRR JIAKLGVSAV RFVEPNNAIT VNTQNEFTTK 6		VKDLSDEERR TLAKICTONT BETTELL	NNTIT VNTONEFTTR
	RFVE	RFVF	1	RFIEF	t t i	スゲン氏が
E	TLAKLGVSAV	TLAKLGVSAV	; ; ; ;	ALAKLGVSAV	TI AKI CITONI	ハゼロハウコンにコーナ
VKDI GREEF	いらしてでである。	VKDLSDEERE	WKDI, SDEBB	3433000 3433000 34330000000000000000000	VKDLSDEERE	
VIEAKRVI, F	11101 K T T T T	> 1 5 4 5 5 5 7 5 5 5 5 5 5 5 5 5 5 5 5 5 5	VIEAKRILEK	, , ,	VIEAKRVLEK	
Hmw3com	Hmw4com		HMWICOM	Hmw.		

1632	ייי סקק אנאאים"	DO SOUNTIE	TNVADDG QQ	a Sindatiny	· 兄 りいつじょうご	TNVADDG QP
	RW) (노 >	TVC) •	RVC
	KACFSSGNGA	K A C II C C C II C A	Apanga inini	RACFSNSDGA		NACE SSGNGA
, , ,	PSSQVTISEG KACFSSGNGA RVCTNIVADA OO	PSSQVTISEG	OO BOOK KACTINAADDG OO	PLSRIVISEG RACFSNSDGA TVCVNIADNC B	PSSOVT TOBO	- ZYYYYADDG QP
	Hmw3com	Hmw4com	Hmm.1		Hmw2com	

kDa 200

116

94

67

43 HMW1

FIG. 11 HMW 2

WESTERN IMMUNOBLOT ASSAY OF PHAGE LYSATES CONTAINING EITHER THE HMW1 OR HMW2 RECOMBINANT PROTEINS. LYSATES WERE PROBED WITH AN *E. COLI-* ABSORBED ADULT SERUM SAMPLE WITH HIGH-TITER ANTIBODY AGAINST HIGH-MOLECULAR-WEIGHT PROTEINS. THE ARROWS INDICATE THE MAJOR IMMUNOREACTIVE PROTEIN BANDS OF 125 AND 120 kDa IN THE HMW1 AND HMW2 LYSATES, RESPECTIVELY.

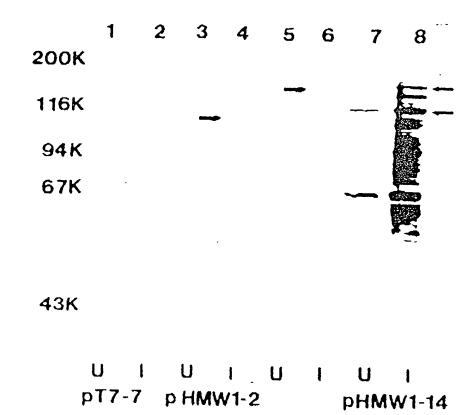


FIG. 12

WESTERN IMMUNOBLOT ASSAY OF CELL SONICATES PREPARED FROM E. COLI TRANSFORMED WITH PLASMID pT7-7 (LANES 1 AND 2) pHMW1-2 (LANES 3 AND 4), pHMW1-4 (LANES 5 AND 6), OR pHMW1-14 (LANES 7 AND 8). THE SONICATES WERE PROBED WITH AN E. COLI-ABSORBED ADULT SERUM SAMPLE WITH HIGH -TITER ANTIBODY AGAINST HIGH - MOLECULAR -WEIGHT PROTEINS. LANES LABELED U AND I REPRESENT SONICATES PREPARED BEFORE AND AFTER INDUCTION OF THE GROWING SAMPLES WITH IPTG, RESPECTIVELY. THE ARROWS INDICATE PROTEIN BANDS OF INTEREST AS DESCRIBED IN THE TEXT.

pHMW1-4

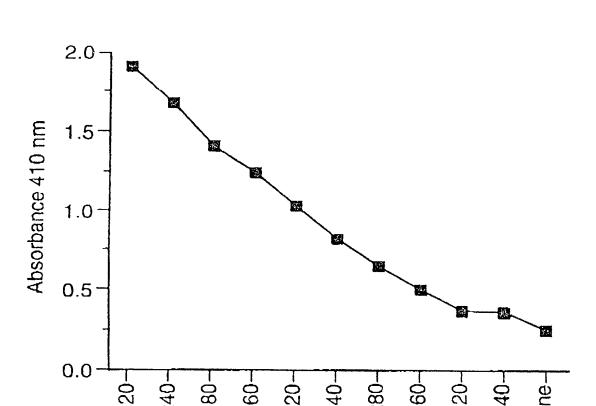


FIG. 13
ELISA WITH rHMW1 ANTISERUM ASSAYED AGAINST PURIFIED FILAMENTOUS HEMAGLUTININ OF B. PERTUSSIS. Ab, ANTIBODY.

Ab Dilutions

200K

116K

94K

67K

43K

5 7 12 14 15 16 17 18

FIG. 14

WESTERN IMMUNOBLOT ASSAY OF CELL SONICATES FROM A PANEL OF EPIDEMIOLOGICALLY UNRELATED NONTYPEABLE H. INFLUENZAE STRAINS. THE SONICATES WERE PROBED WITH RABBIT ANTISERUM PREPARED AGAINST HMW1-4 RECOMBINANT PROTEIN. THE STRAIN DESIGNATIONS ARE INDICATED BY THE NUMBERS BELOW EACH LANE.

200K

116K

94K

67K

43K

5 7 12 14 15 16 17 18

FIG. 15

WESTERN IMMUNOBLOT ASSAY OF CELL SONICATES FROM A PANEL OF EPIDEMIOLOGICALLY UNRELATED NONTYPEABLE H. INFLUENZAE STRAINS. THE SONICATES WERE PROBED WITH MONOCLONAL ANTIBODY X3C, A MURINE IGG ANTIBODY WHICH RECOGNIZES THE FILAMENTOUS HEMAGGLUTININ OF B. PERTUSSIS (13). THE STRAIN DESIGNATIONS ARE INDICATED BY THE NUMBERS BELOW EACH LANE.

1 2 3 4

kDa

200

116

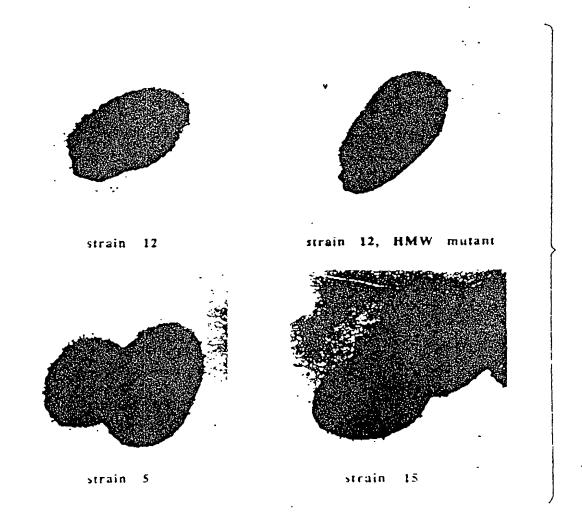
94

67

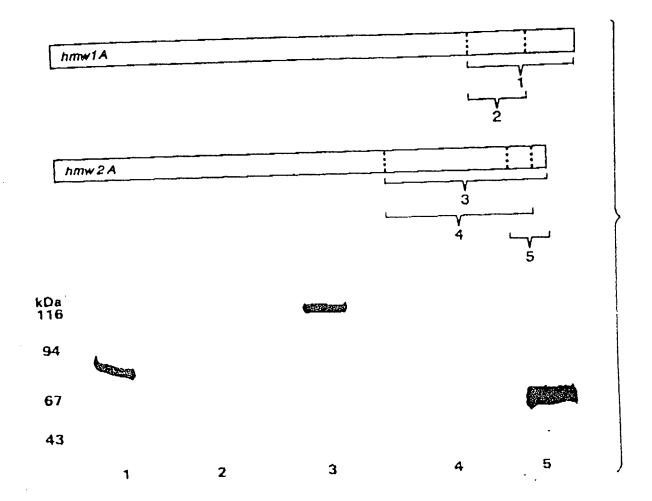
43

FIG. 16

IMMUNOBLOT ASSAY OF CELL SONICATES OF NONTYPABLE H. INFLUENZAE STRAIN 12 DERIVATIVES. THE SONICATES WERE PROBED WITH RABBIT ANTISERUM PREPARED AGAINST HMW-1 RECOMBINANT PROTEIN. LANES: 1, WILD-TYPE STRAIN; 2, HMW-2 MUTANT; 3, HMW-1 MUTANT; 4, HMW-1 / HMW-2 DOUBLE MUTANT.

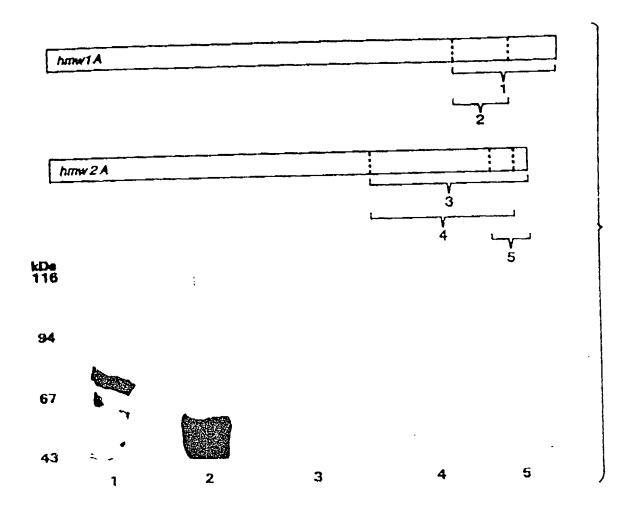


IMMUNOELECTRON MICROSCOPY WITH Mab AD6 FIG.20



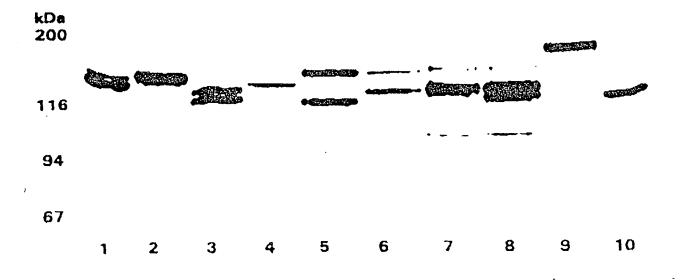
WESTERN IMMUNOBLOT ASSAY WITH Mab AD6 AND HMW1A OR HMW2A RECOMBINANT PROTEINS

FIG.21



WESTERN IMMUNOBLOT ASSAY WITH Mab 10C5 AND HMW1A OR HMW2A RECOMBINANT PROTEINS

FIG.22



WESTERN IMMUNOBLOT ASSAY WITH Mab AD6 AND TEN UNRELATED NONTYPABLE HAEMOPHILUS INFLUENZAE

FIG.23